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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07R 14/705, C12N 15/12		A2	(11) International Publication Number: WO 00/29448
			(43) International Publication Date: 25 May 2000 (25.05.00)
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(22) International Filing Date: 17 November 1999 (17.11.99)			
(30) Priority Data: 10/326255 17 November 1998 (17.11.98) JP 10/364315 22 December 1998 (22.12.98) JP 11/69811 16 March 1999 (16.03.99) JP 11/119299 27 April 1999 (27.04.99) JP 11/138169 19 May 1999 (19.05.99) JP		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING THESE PROTEINS			
(57) Abstract The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs.			

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DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

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TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for genetic diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantity can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like.

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden

potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like have been currently employed as pharmaceuticals. In addition,
5 secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is
10 expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal
15 transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned.
20 It has been clarified that abnormalities of these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the
25 membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which
30 a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of

interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein.
5 After synthesis in the ribosome, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the whole base
10 sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

OBJECTS OF THE INVENTION

15 The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as transformed eukaryotic cells that are capable of expressing these DNAs. This object as well as
20 other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

25 BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02539.

Fig. 2 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02770.

30 Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02869.

Fig. 4 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP02956.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02962.

Fig. 6 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP03014.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10608.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10609.

10 Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10611.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10617.

15 Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02837.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02991.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03063.

20 Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03091.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03092.

25 Fig. 16 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03116.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10618.

Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10619.

30 Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10622.

Fig. 20 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP10625.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02883.

5 Fig. 22 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03140.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10628.

Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10629.

10 Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10635.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10636.

15 Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10640.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10644.

Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10656.

20 Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10672.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03194.

25 Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03219.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03236.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03237.

30 Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03267.

Fig. 36 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP03270.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03298.

5 Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10631.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10658.

Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10663.

10 Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03165.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03266.

15 Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03287.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10665.

Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10669.

20 Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10670.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10671.

25 Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10673.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10675.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10683.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides a DNA encoding the above-mentioned protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150 as well as an expression vector that is capable of expressing such DNA by in vitro translation or in eukaryotic cells and a transformed eukaryotic cell that is capable of expressing such DNA and of producing the above-mentioned protein.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequence of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the

cdNA of the present invention, and then carrying out in vitro translation using this RNA as a template. Alternatively, introduction of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by introducing the translated region of this cdNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector in which the translated region of the cdNA of the present invention is introduced into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cdNA-cloning site, a terminator and the like is constructed. After transformation

of the host cells with this expression vector, the resulting transformant is grown, whereby the protein encoded by the cDNA can be produced in large quantity in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the cell-membrane surface, by introducing the translated region of the cDNA into an expression vector for eukaryotic cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, *Xenopus* oocytes and the like. Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method

known in the art such as the electroporation method, the calcium phosphate method, the liposome method, the DEAE-dextran method and the like.

5 After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated from the culture and purified by a combination of separation procedures known in the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication,
10 enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography and the like.

15 The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments
20 can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the
25 protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be
30 converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where

sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall also come within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for colony or plaque hybridization according to a method known in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-

PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest are synthesized, which are then used as the primers.

5 The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1 summarizes the clone number (HP number), the cells
10 from which the cDNA clone was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID NO	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP02539	Saos-2	4485	647
2, 12, 22	HP02770	HT-1080	1509	350
3, 13, 23	HP02869	KB	3059	206
4, 14, 24	HP02956	KB	2367	213
5, 15, 25	HP02962	KB	2355	595
6, 16, 26	HP03014	Liver	1024	264
7, 17, 27	HP10608	Saos-2	1237	343
8, 18, 28	HP10609	KB	1332	244
9, 19, 29	HP10611	KB	1932	303
10, 20, 30	HP10617	HT-1080	1124	160
31, 41, 51	HP02837	HT-1080	4473	1445
32, 42, 52	HP02991	KB	2630	582
33, 43, 53	HP03063	HT-1080	1472	410
34, 44, 54	HP03091	Liver	1652	483
35, 45, 55	HP03092	Liver	2112	607
36, 46, 56	HP03116	KB	1087	314
37, 47, 57	HP10618	HT-1080	1694	94
38, 48, 58	HP10619	HT-1080	1522	218
39, 49, 59	HP10622	Liver	1591	460
40, 50, 60	HP10625	Liver	1249	216
61, 71, 81	HP02883	KB	4027	392
62, 72, 82	HP03140	HT-1080	2495	497
63, 73, 83	HP10628	HT-1080	1617	417
64, 74, 84	HP10629	WERI-RB	3269	649
65, 75, 85	HP10635	WERI-RB	458	93
66, 76, 86	HP10636	HT-1080	1712	425
67, 77, 87	HP10640	WERI-RB	1055	149
68, 78, 88	HP10644	WERI-RB	1616	396
69, 79, 89	HP10656	PMA-U937	1860	350
70, 80, 90	HP10672	Thymus	783	153
91, 101, 111	HP03194	KB	3438	303

92, 102, 112	HP03219	PMA-U937	1144	283
93, 103, 113	HP03236	HT-1080	2339	488
94, 104, 114	HP03237	HT-1080	1765	182
95, 105, 115	HP03267	Liver	1418	184
96, 106, 116	HP03270	PMA-U937	1211	140
97, 107, 117	HP03298	PMA-U937	1099	153
98, 108, 118	HP10631	WERI-RB	3489	173
99, 109, 119	HP10658	HT-1080	931	75
100, 110, 120	HP10663	PMA-U937	1123	159
121, 131, 141	HP03165	KB	3234	636
122, 132, 142	HP03266	HT-1080	2490	318
123, 133, 143	HP03287	Thymus	1465	82
124, 134, 144	HP10665	HT-1080	917	247
125, 135, 145	HP10669	WERI-RB	1306	206
126, 136, 146	HP10670	WERI-RB	2022	432
127, 137, 147	HP10671	Thymus	1227	306
128, 138, 148	HP10673	Thymus	2210	555
129, 139, 149	HP10675	Thymus	1493	250
130, 140, 150	HP10683	PMA-U937	1264	174

5 The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

10 In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150 shall come within the scope of the present

invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come
5 within the scope of the present invention, as long as the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention also include cDNA
10 fragments (of 10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA
15 fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention
20 may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of
25 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention
30 can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use;

as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern
5 gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source
10 of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of
15 expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example,
20 in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors
25 of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit
30 another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological

fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to
5 isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.
10 Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for
15 commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory
20 Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases
30 the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the

form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

5 Cytokine and Cell Proliferation/Differentiation
 Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or
10 may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of
15 cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165,
20 HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in
25 Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol.
30 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol.

149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as

candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
10 thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly
15 allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

 Using the proteins of the invention it may also be
20 possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
25 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
30 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen
5 functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For
10 example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the
15 transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an
20 activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function
25 in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte
30 antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a

subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class

II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In
10 vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify,
25 among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079,
30 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994;

Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808,
10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology
15 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the
25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells
30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as
5 open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

10 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming
15 cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by
20 inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or
25 other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing
30 protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

25 A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

5 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglestein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are
15 characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.
20 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the
25 ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime
30 reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; 5 Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic 10 or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a 15 desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or 20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or 25 indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing 30 such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-
5 474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such
10 receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules
15 (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors
20 of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among
25 other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing
30 Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987;

Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

5 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

10

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO 98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO 97/33993), the cDNA library of epidermoid carcinoma cell line KB (WO 98/11217) and the cDNA library of liver tissue delivered by the operation (WO 98/21328) were used as the

cdna libraries. Additionally, the cdna libraries constructed from phorbol ester-stimulated histiocytic lymphoma cell line U937 (ATCC CRL 1593) mRNA, human retinoblastoma cell line WERI-RB (ATCC HTB 169) mRNA and human thymus mRNA (Clontech) were also used. Full-length cdna clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cdna bank consisting of the full-length cdna clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cdna clones registered in the homo-protein cdna bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. A clone that has a hydrophobic region being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cdna of the present invention was used for in vitro transcription/translation with a T₇T rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T₇T rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried

out by adding 2.5 μ l of a canine pancreas microsome fraction (Promega) to the reaction system. To 3 μ l of the reaction solution was added 2 μ l of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

10 (3) Expression in COS7

Escherichia coli cells harboring the expression vector for the protein of the present invention were cultured at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μ g/ml of ampicillin, the helper phage M13K07 (50 μ l) was added, and the cells were then cultured at 37°C overnight. Single-stranded phage particles were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 μ l of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

20 The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. 1 x 10⁵ COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 25 37°C for 22 hours in the presence of 5% CO₂. After the medium was removed, the cell surface was washed with a phosphate buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 μ l of the single-stranded phage suspension, 0.6 ml of the 30 DMEM medium and 3 μ l of TRANSFECTAM™ (IBF) was added to the cells and the cells were cultured at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cystine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

10 <HP02539> (SEQ ID NOS: 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP02539 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 188-bp 5'-untranslated region, a 1944-bp ORF,
15 and a 2353-bp 3'-untranslated region. The ORF encodes a protein consisting of 647 amino acid residues and there existed a putative secretory signal at the N-terminus and six putative transmembrane domains at the C-terminus. Figure 1 depicts the hydrophobicity/hydrophilicity profile,
20 obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse frizzled-1 (GenBank
25 Accession No. AF054623). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse frizzled-1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the
30 present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.4% in the entire

region.

Table 2

HP MAEEEEAPKKSRAAGGGASWELCAGALSARLTEEGSGDAGGRRRPPVDPRRLARQLLLLLLW
 ****.*.*.*.*.* * * ****.*.*.*.* * * .*.***.*.*.*.* * .*****
 5 MM MAEEAAPSESRAA-GRLSLELCAEALPGRREEVGHEDTASHRRPRADPRRWASGLLLLLLW
 HP LLEAPLLLGVRAQAAGQGPGQGPQPPPPPPQQQSGQQYNGERGISVPDHGYCQPIS
 ***** ** .*****.*****.*****.*****.*****
 MM LLEAPLLLGVRAQAA----GQVSGPGQAPPQPQQSGQQYNGERGISIPDHGYCQPIS
 HP IPLCTDIAYNQTIMPNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
 10 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 MM IPLCTDMAYNQTIMPNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
 HP EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPPTP
 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 MM EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPPTP
 15 HP SILPEFWTSNPQHGGGGHGGGPGGAGASERKFCPRALKVPSYLNHYHFLGEKDCGAPC
 *****.*****.*.*.*.*.*.*****.*****.*****.*****.*****.*****
 MM SILPEFWTSNGQHGGGGYRGYPGGAGTVERGKFCPRALRVPSYLNHYHFLGEKDCGAPC
 HP EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMMRRFSYPERPIIFLSG
 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 20 MM EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMMRRFSYPERPIIFLSG
 HP CYTAVAVAYIAGFLLEDVRVVCNDKFAEDGARTVAQGTKEGCTILFMMLYFFSMASSIWW
 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 MM CYTAVAVAYIAGFLLEDVRVVCNDKFAEDGARTVAQGTNKEGCTILFMMLYFFSMASSIWW
 HP VILSLTWFLAAGMKWGHEAIEANSQYFHAAWAVPAIKTITILALGQVDGDLVSGVCFVG
 25 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 MM VILSLTWFLAAGMKWGHEAIEANSQYFHAAWAVPAIKTITILALGQVDGDLVSGVCFVG
 HP LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTEKLEKLMVRIGVF
 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 MM LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTEKLEKLMVRIGVF
 30 HP SVLYTVPATIVIACYFYEQAFRDQWERSWAQSCSKSYAIPCPHLQAGGGAPPHPPMSPDF
 *****.*****.*.*.*.*.*.*****.*****.*****.*****.*****.*****
 MM SVLYTVPATIVIACYFYEQAFRDQWERSWAQSCSKSYAIPCPHLQAGGGVPPHPPMSPDF
 HP TVFMIKYLMTLIVGITSGFWIWSGKTLNSWRKFYTRLTNSKQGETTV
 *****.*****.*****.*****.*****.*****.*****.*****.*****.*****
 35 MM TVFMIKYLMTLIVGITSGFWIWSGKTLNSWRKFYTRLTNSKQGETTV

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA010020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02770> (SEQ ID NOS: 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP02770 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 252-bp 5'-untranslated region, a 1053-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was somewhat larger than the molecular weight of 38,274 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human RING zinc finger protein (GenBank Accession No. AF037204). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human RING zinc finger protein (ZN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

Table 3

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA434312) among ESTs. However, since they are partial sequences, it can not be judged whether or

not they encode the same protein as the protein of the present invention.

<HP02869> (SEQ ID NOS: 3, 13, and 23)

5 Determination of the whole base sequence of the cDNA
insert of clone HP02869 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 229-bp 5'-untranslated region, a 621-bp ORF,
and a 2209-bp 3'-untranslated region. The ORF encodes a
10 protein consisting of 206 amino acid residues and there
existed two putative transmembrane domains. Figure 3 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
15 of 22 kDa that was almost identical with the molecular
weight of 22,367 predicted from the ORF.

 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA278247) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
present invention.

25 <HP02956> (SEQ ID NOS: 4, 14, and 24)

 Determination of the whole base sequence of the cDNA
insert of clone HP02956 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 68-bp 5'-untranslated region, a 642-bp ORF,
30 and a 1657-bp 3'-untranslated region. The ORF encodes a
protein consisting of 213 amino acid residues and there
existed three putative transmembrane domains. Figure 4

depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 22 kDa that was almost identical with the
5 molecular weight of 23,902 predicted from the ORF. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
10 protein was similar to the human tetraspan NET-4 (GenBank Accession No. AF065389). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human tetraspan NET-4 (TS). Therein, the marks of -, *, and . represent a gap, an amino
15 acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.8% in the C-terminal region of 119 amino acid residues.

20

Table 4

	HP	MHY
5	TS MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGGFD HP YRYSNAKVSCWYKYLFSYNIIFWLAGVVFLGVGLWAWSEKGVLSDLTKVTRMHGIDPVV	
	TS PVWLFLVVGVMFILGFAGCIGALRENTFLLKFFSVFLGIIFFELELTAGVLAFVFKDWIK HP LVLMVGVVMTLGFAGCVGALRENICLLNFNQCCGAYGPEDWDLNVYFNCSGASYSREKC	
10	TS DQLYFFINNNIRAYRDDIDLQNLIDFTQEYWQCCGAFGADDWNLNIYFNCTDSNASRERC HP GVPFSCCVPDPAQKVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVAGVF *****.***..*.....* *.*****...*.**.*.*****. TS GVPFSCCTKDPADVINTQCGYDARQKPEVDQQIVYITKGCVPQFEKWLQDNLTIVAGIF HP IAISLLQIFGIFLARTLISDIEAVKAGHHF *..***** **..*.....*. TS IGIALLOIFGICLAQNLVSDIEAVRASW	

20 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T05279) among ESTs. However, since they are partial sequences, it can not be judged whether or

25 not they encode the same protein as the protein of the present invention.

<HP02962> (SEQ ID NOS: 5, 15, and 25)

30 Determination of the whole base sequence of the cDNA insert of clone HP02962 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 19-bp 5'-untranslated region, a 1788-bp ORF, and a 548-bp 3'-untranslated region. The ORF encodes a

protein consisting of 595 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 70 kDa that was somewhat larger than the molecular weight of 67,549 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 85 kDa to which sugar chains are presumably attached. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 23. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Thr-Thr at position 75, Asn-Gln-Thr at position 153, Asn-Tyr-Thr at position 237 and Asn-Ser-Ser at position 360).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0584 (GenBank Accession No. AB011156). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0584 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 52.9% in the entire region.

30

Table 5

	HP	MRAARAAPLLQLLLLLGPWLEAAGVAESPL--PAVVLAILARNAEHSL
		*.. .**** *.**..*****.*.*
5	KI	LAWLLLLSSALLREGCRARFVAERDSEDDGEEPVPFPESPLQSPVLVAVLARNAAHTL
	HP	PHYLGALERLDYPRARMALWCATDHNVDNTTEMLQEWLAAGDDYAADVVRPEGEPRFYP
		.* ***.*.*.* *****.*.*.*.* *
	KI	PHFLGCLERLDYPKSRMAIWAATDHNVDNTTEIFREWLKNVQRLYHYVEWRPMDEPESYP
	HP	DEEGPKHWTKERHQFLMELKQEALTFAR-NWGADYILFADTDNLTNNQTLRLIMGQGLP
10		** *****.*.*.*.* **.* *****.*.*.*.* **.*.*.*.*
	KI	DEIGPKHWPTSRFAHVMKLRQAALRTAREKW-SDYILFIDVDNFLTNPQTLNLLIAENKT
	HP	VVAPMLDSQTYYSNFWCGITPQGYRRTAEYFPTKNRQRRGCFRVPVMVHSTFLASLRAEG
		*****.*.* *****.*.*.*.* **.*.*.*.* **.*.*.*.*
	KI	IVAPMLESRLYSNFWCGITPKGFYKRTPDYVQIREWKRTGCFPVMVHSTFLIDLKREA
15	HP	ADQLAFYPPHPNYTWPFDDIIVFAYACQAAGVSVHVCNEHRYGYMNPVKSHQGLEDERV
		.
	KI	SDKLTFYPPHQDYTWTFDDIIVFAFSSRQAGIQMYLCNREHYGYLPIPLKPHQTLQEDIE
	HP	NFIHLILEALVDGPRMQASAHVTRPSKRPSKIGFDEVFVISLARRPDRRERMLASLWEME
		.
20	KI	NLIHVQIEAMIDRPPMEPSQYVSVVPKYPDKMGFDEIFMINLKRRKDRRDRMLRTLYEQE
	HP	ISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQDPYSGRTLTKGEVGCFLSHYSIWEEVVAR
		.
	KI	IEVKIVEAVDGKALNTSQLKALNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSVWKEVIDR
	HP	GLARVLVFEDDVRFESNFRGRLERLMEDVEAEKLSWDLIYLGRKQVN-PEKETAVEGLPG
25		*.*
	KI	ELEKTLVIEDDVRFHQFKKKLMDNIDQAQLDWELIYIGRKRMOVKEPEKAVPNVAN
	HP	LVVAGYSYWTLAYALRLAGARKLLASQPLRRMLPVDEFPLPIMFDQHPNEQYKAHFWRDL
		**.*
	KI	LVEADYSYWTLYGVISLEGAQKLVGANPFGKMLPVDEFPLPVMYNKHPVAEYKEYYESRDL
30	HP	VAFSAQPLLAAPTHYAGDAEWLSDTETSSPWDDDSGRLISWGSQ--KTLRSPRLDLTGS
		****.*.* *****.*
	KI	KAFSAEPLLIYPHTYTGQPGYLSDTETSTIWDNETV-ATDWDRTTHAWKSRKQSRISNAK
	HP	SGHSLQPQRDEL
	*
35	KI	NTEALPPPTSLDTVPSRDEL

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA358896) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03014> (SEQ ID NOS: 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP03014 obtained from cDNA library of human liver revealed the structure consisting of a 26-bp 5'-untranslated region, a 795-bp ORF, and a 203-bp 3'-untranslated region. The ORF encodes a protein consisting of 264 amino acid residues and there existed one putative transmembrane domain. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was somewhat larger than the molecular weight of 28,471 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse WW domain-binding protein 1 (GenBank Accession No. U40825). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse WW domain-binding protein 1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

5

Table 6

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W24575) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10608> (SEQ ID NOS: 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10608 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 23-bp 5'-untranslated region, a 1032-bp ORF, and a 182-bp 3'-untranslated region. The ORF encodes a protein consisting of 343 amino acid residues and there existed five putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 37 kDa that was somewhat smaller than the molecular weight of 40,584 predicted from the ORF. When expressed in COS7 cells, an expression product of about 36 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35406) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10609> (SEQ ID NOS: 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10609 obtained from cDNA library of the human epidermoid carcinoma cell line KB revealed the structure consisting of a 38-bp 5'-untranslated region, a 735-bp ORF, and a 559-bp 3'-untranslated region. The ORF encodes a protein consisting of 244 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 8 depicts the hydrophobicity/hydrophilicity

profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,756 predicted from the ORF.

5 When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Mycobacterium tuberculosis

10 hypothetical protein Rv1147 (GenBank Accession No. Z95584). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Mycobacterium tuberculosis hypothetical protein Rv1147 (MT). Therein, the marks of -, *, and . represent a gap, an amino

15 acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.7% in the entire region.

20

Table 7

[illegible]

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T60981) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP10611> (SEQ ID NOS: 9, 19, and 29)

30 Determination of the whole base sequence of the cDNA insert of clone HP10611 obtained from cDNA library of the human epidermoid carcinoma cell line KB revealed the structure consisting of a 37-bp 5'-untranslated region, a 912-bp ORF, and a 983-bp 3'-untranslated region. The ORF

encodes a protein consisting of 303 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was somewhat smaller than the molecular weight of 33,856 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 36 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34. When expressed in COS7 cells, an expression product of about 35 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the 218 amino acid residues at the C-terminus of the protein matched with the amino acid sequence of human glucosidase II (SWISS-PROT Accession No. Q06003). However, no similarity was observed at the N-terminal portion.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H14054) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10617> (SEQ ID NOS: 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10617 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 72-bp 5'-untranslated region, a 483-bp ORF, and a 569-bp 3'-untranslated region. The ORF encodes a protein consisting of 160 amino acid residues and there existed four putative transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 17 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H67672) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02837> (SEQ ID NOS: 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP02837 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 44-bp 5'-untranslated region, a 4338-bp ORF, and a 91-bp 3'-untranslated region. The ORF encodes a protein consisting of 1445 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 150 kDa that was almost identical with the molecular weight of 161,657 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 22. In addition, there exist in the amino acid sequence of this protein 18 sites at which N-glycosylation
5 may occur.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -2 macroglobulin (SWISS-PROT Accession No. P01023). Table 8 shows the comparison
10 between amino acid sequences of the human protein of the present invention (HP) and the human α -2 macroglobulin (MG). Therein, the marks of - and * represent a gap and an amino acid residue identical with that of the protein of the present invention, respectively. The both proteins shared a
15 homology of 29.5% in the entire region.

Table 8

	HP	MQGPPLL--TAAHLLCVCTAALA-VAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVT
		* * * * * * * * * * *
5	MG	MGKNKLLHPSLVLLLLVLLPTDASVSGKPQYMLVP-SLLHTETTEKGCVLLSYLNETVT
	HP	VKAELLKTASN-LTVSVLEAE-GVFEKGSFKTLTLPPLNSADEIYELRVGTGRTODEIL
		* * * * * * * * * * *
	MG	VSASLESVRGNRSLFTDLEAENDVLHCVAF---AVPKSSSNEEVMFLTVQVKGPTQ---E
	HP	FSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLIL--IKDPKS
10		* * * * * * * * * * *
	MG	FKKRTTVMVKNEDSLVFVQTDKSIYKPGQTVKFRVSMDFHP-LNELIPLVYIQDPKG
	HP	NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQ-VNDQTYYSQSFQVSEYVLPKFEVT
		* * * * * * * * * * *
	MG	NRIAQWQSFQLEGGLKQFSFPLSSEPFQGSYKVVVQKKSGRTEHPFTVEEFVLPKFEVQ
15	HP	LQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVT----LTFLPLSFWGKKKNITKTFKING
		* * * * * * * * * * *
	MG	VTVPKIITILEEEMNVSVCGLYTYGKVPVGHVTVSICRKYSDASDCHGEDSQAFCEKFSG
	HP	SANFSFNDEEMKNVMDSSNGLSEY-LDLSFPGPVEILTTVTESVTG----ISRNVSTNVF
		* * * * * * * * * * *
20	MG	QLNSHGCFYQQVKTQVQLKRKEYEMKLHTEAQIQEEGTVVELTGRQSSEITRTITKLSEF
	HP	FK--QHDYIIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVITVTQRNYTEY
		* * * * * * * * * * *
	MG	VKVDSHFRQGIFFGQVRLVDGKGVPPIPNKVIFIRGN-----EANYYSNATTEHGLV
	HP	WGSNSNGNQKMEAVQKINYTVPSGTFKIEFPILEDSSSELQKAYFLGSKSSMAVHSLFK
25		* * * * * * * * * * *
	MG	QFSINTTN-VMGTSITVRVNYKDRSPCYGYQWVSEEHEEAHTAYLVFSPSKSFVHLEPM
	HP	S--PSKTYIQLKTRDENIKVGSPELVVSGNKRLKELSYMVVSRGQLVAVGKQ--NSTMF
		* * * * * * * * * * *
	MG	SHELPCGHTQTVQAHYILNGGTLGLKLSFYYLIMAKGGIVRTGTHGLLVKQEDMKGHF
30	HP	S-LTPENS-WTPKACVIVYYIEDDGEIISDVLKIPVQLVFNKIKLYWSKVKAEPSEKVS
		* * * * * * * * * * *
	MG	SISIPVKSIDIAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAH
	HP	LRISVT-QPDSIVGIVAVDKSVNLMNASNDITMENNVHEL-ELYNTG-----
		* * * * * * * * * * *
35	MG	LR--VTAAPQSVCALRAVDQSVLLMKPDAELSASSVYNLLPEKDLTGFPGLNDQDDEDC

HP -----YYLGMFMNSFAVFQE-CGLWVLT DANL---TKDYIDGVYDNAEYAERFMEENEG
* * * * *
MG INRHNVYINGITYTPVSSSTNEKDMYSFLEDMGLKAFTNSKIRKPKMCPQLQQYEMHGPEG
HP HIV-----DIHDFSLGSSPH---VRKHFPETWIWLDTNMGSRITYQEFVTVPDSI
5 * ** *** ***** * * *****
MG LRVGFYESDVMGRGHARLVHVEEPHTETVRKYFPETWIWDLVVVNSAGVAE VGVTVPDTI
HP TSWVATGFVISED LGLGLTTTPVELQAFQPFIFLNL PYSVIRGEEFALEITIFNYLKDA
* * * * *
MG TEWKAGAFCLSEDAGLGISST-ASLRAFQPFVELTMPYSVIRGEAFTLKATVLNLYPKC
10 HP TEVKVII EKSDKFDILMTSSE-----INATGHQ-QTLLVPSEDGATVLFPIRPHL--GE
* * * * *
MG IRVSVQLEASPAFLAVPVEKEQAPHICANGRQTVSWAVTPKSLGNVNFTVSAEAL ESQE
HP IPITVTALSP--TASDAITQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPN
* * * * *
15 MG LCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSLL---CPSGGEVSEELSLKLPPN
HP TVTGSEVRQITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLT KKKQLTD
* * * * *
MG VVEESARASVSVLGDILGSAMQNTQNLQMPYGCGEQNMVLFAPNIYVLDYLN ETQQLT
HP NLKEKALSFMROGYQRELLYQREDGSFSAFG--NYDPSGSTWLSAFVLR CFLEADPYIDI
20 * * * * *
MG EVKSKAIGYLN TGYQRLNYKH YDGSYSTFGERYGRNQNTWLTAFVLKTF AQARAYIFI
HP DQNVLHRTYTWLKGHQKSNGEFWD PGRVIHSELQGGNKSPVTLTAYIVT SLLGYRKYQPN
* * * * *
MG DEAHITQALI WLSQRQKDN GCFRSSGSLNNAIKGGVEDEVTL SAYITIALLEIPLTVTH
25 HP IDVQESIHFLES-----EFSRGISDNYTLALITYALSSVG-SPKAKEALNMLTWRAEQE
* * * * *
MG PVVRNALFCLES AWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKK
HP GGMQFW-----VSSSKLSDSWQPRSLDIEVAAYALLSHFLQFQ--TSE-----GIPIMRW
* * * * *
30 MG DNSVHWERPQKPKAPVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTS EDLTSATNIVKW
HP LSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVTG PSS-PSPVKFLIDTHN
* * * * *
MG ITKQONAQGGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNN
HP RLLLOTAELAVVQPTAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNOEAFDL DVA
35 ***** * * * * *

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MG RLLQVSL-PELPGEYSMKVTGEGCVYLQTSCLKYN----ILPEKEEFPFALGVQTLPT
HP VKENK-DDLNHVDLNVCTSFSGPGRSGMALMEVNLISGFMVPSEAISETVKKVEYDHG
      * *      * *      *      * * *      *      * *      * *
MG CDEPKAHTSFQISLSVSYTGS-RSASNMAIVDVKMVSGF-----IPLKPTVKMLE----
5  HP KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYEPRRQAVRSYNSEVKLSSCD
      * *      *      * * *      *      *      * *      *
MG ----RSNHVSRTEVSSNHVLIYLDKVSNTLSLFFTVLQDVP----VR-----D
HP LCSDVQGCPCEDGASGSHHSSVIFIFCFKLLYFMELWL
      *      *      * * *
10 MG L---KPAIVKVYDYYETDEFAIAEYNAPCSKDL----GNA

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W33075) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20 <HP02991> (SEQ ID NOS: 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02991 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 81-bp 5'-untranslated region, a 1749-bp ORF, and a 800-bp 3'-untranslated region. The ORF encodes a protein consisting of 582 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 66 kDa that was somewhat larger than the molecular weight of 64,244 predicted from the ORF. In

this case, the addition of a microsome led to the formation of a product of 78 kDa to which sugar chains are presumably attached. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 27. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Gly-Thr at position 70, Asn-Gly-Thr at position 182, Asn-Gly-Ser at position 294, Asn-His-Thr at position 310, Asn-Gly-Thr at position 352, Asn-Glu-Thr at position 393 and Asn-Cys-Ser at position 407).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FKBP65-binding protein (GenBank Accession No. L07063). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FKBP65-binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 88.8% in the entire region.

Table 9

	HP	MFPAGPPSHSLLRLPLLQLLLLQVAVGRGLGRASPAGGPLEDVVIERYHIPRACPREVQ
		** .*.***. *...*.***** .*.***.*****.*****.*****
5	MM	MFLVGSSSHTLHRVRILPLLLL-LQTLERGLGRASPAGAPLEDVVIERYHIPRACPREVQ
	HP	MGDFVRYHYNGTFEDGKKFDSSYDRNTLVAIVVGVRGLITGMDRGLMGMCVNERRRLIVP
		*****.*****.*****.*****.*****.*****.*****.*****
	MM	MGDFVRYHYNGTFEDGKKFDSSYDRSTLVAIVVGVRGLITGMDRGLMGMCVNERRRLIVP
	HP	PHLGYGSIGLAGLIPPDATLYFDVVLDDVWNKEDTVQVSTLLRPPHCPRMVQDGDVRYH
10		*****.*****.*****.*****.*****.*****.*****.*****
	MM	PHLGYGSIGVAGLIPPDATLYFDVVLDDVWNKADTVQSTILLRPPYCPRMVQNSDFVRYH
	HP	YNGTLLDGTSTFDTSSYKGGTYDITYVGSGLIKGMDQGLLMCPGERRKIIIPPFLAYGEK
		*****.***.***.*****.*****.*****.*****.*****
	MM	YNGTLLDGTGFDNSYSRGGTYDITYIGSGWLKMGMDQGLLMCPGERRKIIIPPFLAYGEK
15	HP	GYGTVIPPQASLVFVLLIDVHNPKDAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDG
		*****.***.*****.*****.*****.*****.*****.*****
	MM	GYGTVIPPQASLVFVLLIDVHNPKDTVQLETLELPQGCVRRAVAGDFMRYHYNGSLMDG
	HP	TLFDSSYSRNHTYNTYIGQGYIIPGMDQGLQGACMGERRRITIPPHLAYGENGTGDKIPG
		*****.*****.*****.*****.*****.*****.*****.*****
20	MM	TLFDSSYSRNHTYNTYIGQGYIIPGMDQGLQGACIGERRRITVPPHLAYGENGTGDKIPG
	HP	SAVLIFNVHVIDFHNPAADVVEIRTLRPSSETCNETTKLGDFVRYHYNCSSLDDGTQLFTSH
		*****.*****.***.***.*****.***.***.*****.*****.***.***
	MM	SAVLIFDVHVIDFHNPSDPVEIKTLRPPENCNETSKIGDFIRYHYNCSSLDDGTRLFSSH
	HP	DYGAPQEATLGANKVIEGLDTGLQGMCGERRQLIVPPHLAGESGARGVPGSAVLLFEV
25		**.****.*****.*****.*****.*****.*****.*****
	MM	DYEAPQEITLGANKVIEGLDRGLQGMCGERRQLIVPPHLAGENGARGVPGSAVLLFEV
	HP	ELVSREDGLPTGYLFVWHKDPPANLFEDMDLNKDGEPPEEFSTFIKAQVSEGKGRMLPG
		*****.***.***.*****.*****.*****.*****.*****
	MM	ELVSREDGLPTGYLFVWYQDPSTSLFEDMDLNKDGEPPEEFSSFIKAQVNEGKGRMLPG
30	HP	QDPEKTIGDMFQNDQDRNQDGKITVDELKLSDEDEERVHEEL
		..*****.*****.*****.*****.*****
	MM	QDPDKTISDMFQNDQDRNQDGKITAEELKLSDEDQERVHEEL

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA308536) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03063> (SEQ ID NOS: 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP03063 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 88-bp 5'-untranslated region, a 1233-bp ORF, and a 151-bp 3'-untranslated region. The ORF encodes a protein consisting of 410 amino acid residues and there existed a putative transmembrane domain at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was almost identical with the molecular weight of 45,786 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse AUP1 (GenBank Accession No. U41736). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse AUP1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.2% in the entire region.

Table 10

HP MELPSGPGPERLFDShRLPGDCFLLLVLLLlYAPVGFCLLVLRLFLGLHVFLVSCALPDSV
 ** * .*****. * ****.*****.*****.*****
 5 MM MEPPAPGPERLFDShRLPSDGFLLLALLlYAPVGLCLLVLRLFLGLHVFLVSCALPDSV
 HP LRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDHNIVNLLTTCSTPLLNSPP
 *****.*****
 MM LRRFVVRTMCAVLGLVARQEDSGLRDHRVRVLISNHVTPFDHNIVNLLTTCSTPLLNSPP
 HP SFVCWSRGMEMNGRGELVESLKRFCASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFS
 10 *****. * *****.*****
 MM SFVCWSRGMEMDRRVELVESLKKFCASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFS
 HP IQDVVQPLTLQVQRPLVSVTVSDASWVSELLWSLFPFTVYQVRWLRPVHRQLGEANEFF
 *****.*.*****.
 MM IQDVVQPLTLQVQRPLVSVTVSDASWVSELLWSLFPFTVYQVRWLHPIRRQLGEESEEF
 15 HP ALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRPQSAQSSFPSPGSPDPVQLATL
 *****.*****.*****.*.***.***.
 MM ALRVQQLVAKELGQIGTRLTPADKAEHMKRQRHPRLRPQSVQSSFPSPSPSSDVQLTTL
 HP AQRVKEVLPHVPLGVIQRDLAKTGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKF
 *.*****.*****.*****.*.*.***.*.***.
 20 MM AHRVKEVLPHVPLNVIQRDLARTGCVDLTITNLLEGAVAFMPEDVTEGSQSPAPSAKPF
 HP PSSGPVTPQPTALTFAKSSWARQESLQERKQALYFYARRRFTERRAQEAD
 ****.*****.***.
 MM PSSGLATPOPTALTFAKSSWARQESLQERKQALYFYARRRFRERQAQAE

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA131932) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP03091> (SEQ ID NOS: 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03091 obtained from cDNA library of human liver revealed the structure consisting of a 16-bp 5'-untranslated region, a 1452-bp ORF, and a 184-bp 3'-untranslated region. The ORF encodes a protein consisting of 483 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human OS-9 protein (SWISS-PROT Accession No. Q13438). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OS-9 protein (OS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.8% in the N-terminal region of 281 amino acid residues. The positions of eight cysteines were conserved between the two proteins.

Table 11

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HP MEEGGGGVRSIVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGV
      .*. . . . . **.* *** . . . . . *. . . . . ****. *
5  OS      MAAETLLSLLGLLLL-GLLLPASLTGGVGSLNLEELSEMRYGIEILPLPVMGGQ
HP YKEDNYVIMTTAHKEKYKCILP----LVTSGDEEEEEKDYKGPNPRELLEPLFKQSSCSYR
      . . . . . ** . . . . . * . . . . . . . . . . . . . . . . * . .
OS SQSSDVVIVSSSKYKQRYECRLPAGAIHFQREEREETPAYQGPPIPELLSPM-RDAPCLLK
HP IESYWTYEVCHGKHIRQYHEEKETGQKINIHEYVLGNMLAKNLLFEKEREAEKEKSNEI
10      . . . . . ***** *. . . . . ***** * . . . . . * . . . . . *** . . . . . . . . . . . **.*
OS TKDWWTYEFCYGRHIQQYHME-DSEIKGEV--LYLG-----YYQSAFD-----WDEET
HP PTKNIEGQMTPIYPVGMGNGTPCSLKQNRPRSSTVMYIC---HPESKHEILSVAEVTTC
      . . . . . . . . . . . * . . . . . ***. *. * . . . . . * . . . . . * . . . . . * . . . . . * . .
OS AKASKQHRLKRYHSQTYGNGSKCDL-NGRPREAQVRFLEDEGAGISGDYIDRVDEPLSCS
15 HP YEVVILTPLLCSHPKYRFRASPV-NDIFCQ-SLPGSPFKPLTLRQLEQQEEILRVPFRN
      * . . . * ** **.* ** * . . . * . . . . . ** . . . . . ** . . .
OS YVLTIRTPRLCPHPLLRPPPSAAPQAILCHPSLQPEEYMAVQORQADSKQYGDKIIIELO

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20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA313678) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP03092> (SEQ ID NOS: 35, 45, and 55)

Determination of the whole base sequence of the cDNA insert of clone HP03092 obtained from cDNA library of human liver revealed the structure consisting of a 19-bp 5'-untranslated region, a 1824-bp ORF, and a 269-bp 3'-untranslated region. The ORF encodes a protein consisting of

607 amino acid residues and there existed at least six putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat liver-specific transport protein (GenBank Accession No. L27651). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat liver-specific transport protein (RN). Therein, the marks of - and * represent a gap and an amino acid residue identical with that of the protein of the present invention, respectively. The both proteins shared a homology of 70.0% in the entire region.

Table 12

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HP MGFEELLEQVGGFGPFQLRNVALLALPRVLLPLHFLLPIFLAAVPAHRCALPGAPANFSH
    **** ** ***** * **** * **** * **** * **** * **** *
5  RN MGFEDLLDKVGGFGPFQLRNLVLMALPRMLLPMHFLLPVFMAAVPAHHCALPGAPANLSH
HP QDVWLEAHLPREPDGTLSSCLRFAYPQALPNTTLGEERQSRGELEDEPATVPCSQWEYD
    ** ***** ** ***** ** * * ** * * *****
RN QDLWLEAHLPRETDGSFSSCLRFAYPQTVPNVTLGTEVSNSGEPEGEPLTVPCSQWEYD
HP HSEFSSTIATESQVGIYIIHLEVECRWRQSPWEAAGRGLPWEEAEAAGLGRDKVSYSPSW
10 *****
RN RSEFSSTIAT-----
HP RESLGGLLSGMEWDLVCEQKGLNRAASTFFFAGVLVGAVAFGYLSDRFGRRRLLLVAYVS
    ***** * ** * * ***** *****
RN -----EWDLVCCQQRGLNKITSTCFFIGVLVGAVVYGYLSDRFGRRRLLLVAYVS
15 HP TLVLGLASAASVSVMFAITRTLTSALAGFTIIVMPLELEWLDVEHRTVAGVLSSTFWT
    ***** * * * * ***** ***** * **
RN SLVLGLMSAASINYIMFVVRTLTGSALAGFTIIVLPLELEWLDVEHRTVAGVISTVFW
HP GGVMLLALVGYLIRDWRWLLAVTLPCAPGILSLWVPESARWLLTQGHVKEAHRYLLHC
    *** ***** ***** * * * * ***** * ** *
20 RN GGVLLLALVGYLIRSWRWLLLAATLPCVPGIISIWWVPESARWLLTQGRVEEAKKYLLSC
HP ARLNGRPVCEDSFSQEAVSKVAAGERVVRPSYDLFRTPLRHISLCCVVWFVGNFSY
    * ***** * * **** * ** ***** *****
RN AKLNGRPVGEGLSQAELNNVVTMERALQRPYDLFRTSQLRHISLCCMMVWFVGNFSY
HP YGLSLDVSGGLNVYQTQLLFGAVELPSKLLVYLSVRYAGRRLTQAGTLLGTALAFGTRL
25 *** ***** ** * * ***** * * * * *
RN YGLTLDVSGGLNVYQTQLLFGAVELPSKIMVYFLVRLGRRLTEAGMLLGAALTFTGTS
HP LVSSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSELYPTVLRQTGMGLTALVGRLLGSLAP
    *** * * * * ***** ***** * * *
RN LVSLETKSWITALVVVGKAFSEAAFTTAYLFTSELYPTVLRQTGLGLTALMGRLGASLAR
30 HP LAALLDGVWLSLPLKTYGGIALLAAGTALLLPETROAQLPETIQDVERKSAPTSLQEEEM
    ***** * * ***** ***** * *
RN LAALLDGVWLLLPKVAYGGIALVAAGTALLLPETKKAQLPETIQDVERK---STQEE--
HP PMKQVQN
35 RN -----DV

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI016020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03116> (SEQ ID NOS: 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP03116 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 32-bp 5'-untranslated region, a 945-bp ORF, and a 110-bp 3'-untranslated region. The ORF encodes a protein consisting of 314 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 20. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 167, Asn-Asn-Ser at position 200 and Asn-Ile-Ser at position 273).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human Prostatic (SWISS-PROT Accession No. Q16651). Table 13 shows the comparison between amino acid sequences of the human protein of the present

invention (HP) and the human Prostatin (PR). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.8% in the entire region.

Table 13

10	HP	MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPW
		..*.* . . * ** *. ..*** . .***.*.* *.*
	PR	MAQKGVLPQGLGAVAILLYLGLLRSGTG-AEGAEAPCG-VAPQARITGGSSAVAGQWPW
	HP	QGSLRLWDSHVCVSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAY
		* *. . **** *.*.*.*.*.*.*.*.*. *.*. . *. .
15	PR	QVSITYEGVHVCGLVSEQWVLSAAHCF---PSEHHKEAYEVKLGA-HQLDSY---SED
	HP	YTRYFVSNIIYLSPRYLGNSPY-DIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVT
	* *.** ... ***** *.*.*.*.*.*.*.*.*. * * . * **
	PR	AKVSTLKDIIIPHSYLQEGSQGDIALQLSRPITFSRYIRPICLPAANASFPNGLHCTVT
	HP	GWGYIKEDEALPSPHTLQEVQVAIINNSMCNHLF-LKYSFRKDIF--GDMVCAGNAQGGK
20		****. . . * .*.***.*.*.*.*.*.*.*. ** *. . . . * .***** ..***
	PR	GWGHVAPSVSLLTPKPLQQLLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGK
	HP	DACFGDSGGPLACNKNGLWYQIGVSVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMS
		*** *****.* .***** .*.***** .** .***** * .****. ...
	PR	DACQGDSSGGLSCLPVEGLWYLTGIVSWGDCGARNRPGVYTLASSYASWIQSKVTELQPR
25	HP	QPDPSWPLLFFPLLWALPLLGPV
	PR	VVPQTQESQPDNLGSHLAFSSAPAQGLLRPILFLPLGLALGLLSPWLSEH

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159101) among ESTs. However, since they are partial sequences, it can not be judged whether or

not they encode the same protein as the protein of the present invention.

<HP10618> (SEQ ID NOS: 37, 47, and 57)

5 Determination of the whole base sequence of the cDNA
insert of clone HP10618 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 215-bp 5'-untranslated region, a 285-bp ORF,
and a 1194-bp 3'-untranslated region. The ORF encodes a
10 protein consisting of 94 amino acid residues and there
existed a putative transmembrane domain at the N-terminus.
Figure 17 depicts the hydrophobicity/hydrophilicity profile,
obtained by the Kyte-Doolittle method, of the present
protein. In vitro translation resulted in formation of a
15 translation product of 10 kDa that was almost identical with
the molecular weight of 9,709 predicted from the ORF.

 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA287125) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
present invention.

25 <HP10619> (SEQ ID NOS: 38, 48, and 58)

 Determination of the whole base sequence of the cDNA
insert of clone HP10619 obtained from cDNA library of the
human fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 11-bp 5'-untranslated region, a 657-bp ORF,
30 and a 854-bp 3'-untranslated region. The ORF encodes a
protein consisting of 218 amino acid residues and there
existed a putative transmembrane domain at the N-terminus.

Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43089) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10622> (SEQ ID NOS: 39, 49, and 59)

Determination of the whole base sequence of the cDNA
15 insert of clone HP10622 obtained from cDNA library of the human liver revealed the structure consisting of a 43-bp 5'-untranslated region, a 1383-bp ORF, and a 165-bp 3'-untranslated region. The ORF encodes a protein consisting of 460 amino acid residues and there existed a putative
20 secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the
25 mature protein starts from serine at position 17. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Ser-Ser at position 23, Asn-Met-Ser at position 115, Asn-Glu-Thr at position 296 and Asn-Tyr-Thr at position 357).

30 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human angiopoietin-1 (GenBank

Accession No. U83508). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human angiopoietin-1 (AN). Therein, the marks of -, *, and . represent a gap, an amino acid
5 residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 28.2% in the entire region and a homology of 39.1% in the C-terminal region of 215 amino
10 acid residues.

Table 14

HP	MFTIKLLLFIVPLVISS
5	AN MTVFLSFAFLAAILTHIGCSNQRRSPENSGRRYNRIQHGCAYTFILPEHDGNCRESTD HP RIDQDNSSFDLSPEPKSRFAMLDDVKILANGLLQLGHGLKDF-VHKTKGQINDIFQKLN ** . . . * * . . . * . . . * . . . * . . .
10	AN QYNTNALQRDAPHVEPDFSSQKLQHLEHVMENYTQWLQKLENYIVENMKSEMAQI-QQNA HP IFDQSFYDLSLOTSEIKEEEKELRR-TTYKLQVKNEEVKNMSLELNSKLESILLEEKILLQ * . . * * . . . * . . . * . . . * . . . * . . . * . . . AN VQNHATATMLEIGTSLLSQTAEQTRKLTQVETQVLNQTSLRLEIQLENSLSTYKLEKQLLQ HP QKVKYLE-EQLTNLIQNPETPEHPEVTSKLTQVFKQDNQSIKDLLQTVEDQYKQLNQOHS * . . * . . . * * . . . * . . . * . . . * . . . * . . . * . . .
15	AN QTNEILKIHEKNSLLEHKILEMEGKHKEELDTLKEEKEN-LQGLVTRQTYIIQELEKQLN HP QIKEIENQLRRTSIQEPTEISLSSKPRAPRTTFFLQNEIRNVKHDGIPAECTTIYNRGE * . . * * * . . . * . . . * . . . AN RATTNNSVLQKQQL-ELMDTVHNLVNLCTKEGVLL--KGGKREEEKPFR-DCADVYQAGF HP HTSGMYAIRPSN-SQVFHVYCDV-ISGSPWTLIQHRIDGSQNFNETWENYKYGFGRLDGE * . . * * . . . * . . . * . . . * . . . * . . .
20	AN NKSGIYTIYINNMPKPKVFCNMDVNGGGWTVIQHREDGSLDFQRGWKEYKMGFGNPSGE HP FWLGLEKIYSIVKQSNYVLRIELEDWKDNKHYYIEY-SFYLGNHETNYTLHLVAITGNVPN * * . . . * . . . * . . . * . . . AN YWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGHTGTAGK HP AIP-ENKDLVFSTWDHKAKGHF-NCPEGYSGGWWHDECGENNLNGKYNKPRAKSPERR * . . * * . . . * . . . * . . . * . . . * . . .
25	AN QSSLILHGADFSTKDADNDNCMCKCALMLTGGWWF-DACGPSNLNGMFY--TAGQNHGKL HP RGLSWKSQNGRLYSIKSTKMLIHPTDSESEF * . . * * . . . * . . . * . . . * . . . * . . .
30	AN NGIKWHYFKGPSYSLRSTTMMIRPLDF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. R86161) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP10625> (SEQ ID NOS: 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10625 obtained from cDNA library of the human liver revealed the structure consisting of a 133-bp
10 5'-untranslated region, a 651-bp ORF, and a 465-bp 3'-untranslated region. The ORF encodes a protein consisting of 216 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
15 Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R59052) among ESTs. However, since
20 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02883> (SEQ ID NOS: 61, 71, and 81)

25 Determination of the whole base sequence of the cDNA insert of clone HP02883 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 191-bp 5'-untranslated region, a 1179-bp ORF, and a 2657-bp 3'-untranslated region. The ORF encodes a
30 protein consisting of 392 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CET24F1.2 (GenBank Accession No. Z49912). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CET24F1.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.4% in the N-terminal region of 178 amino acid residues.

Table 15

20 HP MEGVSALLARCPTAGLAGGLGVTACAAAGVLLYRIARRMKPHTMVCNWFNCDTLVPYG
 * * * * * *
 CE MEVAAAVGVIAVPIYK-AIRPR-IKTSVECWFCRKSTKVEYQ
 HP NRNCWDCPHCEQYNGFQENG DYKNPIPAQ-----YLEHLNHVSVSSAPSLRDP-SQPQQ
 25 * * * * * * * * * * . . .
 CE QRNSFTCPSCQYNGFTEDGDYNNRIPGQAWTTPKRYCEPGKMQSEKPSFTLDRFGGVNM
 HP WVSSQVLLCKRCNHHQTTIKQLAAFAPREEGRYDEEVEVYRHHLEQMYKLCRPCQAAVE
 . . * . * * * * . * * * . . .
 CE SPKASNGLCSECNLGQEIIMNKVAEFEPIDEDRWNEELEDYRYKLERYQLCPRCTIQVH
 30 HP YYIKHQNRQLRALLSHQFKRREADQTHAQNFSSAVKSPVQVILLRALAFLACAFILLTTA
 * . . * . .
 CE GKLEEDKKKY-SYLLKVYKYLKHAIGSTLREVMNNQKRSRFFFAAGGSTCEALHFGCLIS

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
5 example, Accession No. F11409) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03140> (SEQ ID NOS: 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP03140 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 29-bp 5'-untranslated region, a 1494-bp ORF,
15 and a 972-bp 3'-untranslated region. The ORF encodes a protein consisting of 497 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
20 translation resulted in formation of a translation product of 51 kDa that was almost identical with the molecular weight of 54,245 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
25 protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC50D2 (GenBank Accession No. AF040642). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELC50D2
30 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the N-terminal region of 393 amino acid residues.

Table 16

5

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HP MALWRGSAYAGFLALAVGCVFLLEPELPGSALRSLWSSLCIGPAPAPPGPVSPEGRLAA
* * . . .
CE MFSETFVPSIFSYPKXRLHLSVLFVIVPYWYSYNDQHRLSSYSVETAMFLS
10 HP WDALIVRPVRRWRRVAVGVNACVDVVLSGVKLLQALGLSPGNKGDHSILHSRNDLEEAFI
* . * . * . . . . . * * * . . . * . . . * . . . * . . .
CE WERAIVKPGAMFKKAVIGFNCNVDLIVSGVRVVDALNTTCSEKQDETLETADLHQTF
HP HFMWKGAAAERFFSDKETFDIAQVASEFPGAQHYVGGNAALIGQKFAAN-SDLKVLLCG
* . . * . . . . . * . . . . . * . . . . . * . . . * . . .
15 CE HFFQRGAAAERYMSSSEDQFNLLVAESEASTRSHHHIGGNAALMADRIAANFPSTEVYLVG
HP PVGPRLLHELLDDNVFVPPESLQEVDEFHLILEYQAGEEWGQLKAPHANRFIFSHDLSNGA
* . * . . * . . . * . . . * . . . * . . . * . . . * . . .
CE PIGPRSQALLHPSVKRTNSTRILKDELHVILEYKQGEILGDWVAPSSSRFITSHDHFSGS
HP MNMLEVFVSSLEEFQPDVLVLSGLHMEGQSKELQKRRLLEVVTISIDIPTGIPVHLELA
20 * . . * . . . . * . . . . . * . . . . . * . . . . . * . . . . .
CE MVMEMFFKAIAQFRPDLVVITGVHLLFQSKEMRQEKMRLLIKRNLQIPPKVPIHLELG
HP SMTNRELMSSIVHQQVFAVTSGLNEQELLFLTQSASGPH-SSLSSWNGVPDVGMSDI
* . . . * . . . * . . . * . . . * . . . * . . . * . . .
CE SLAD-EIFSTDVINKILPYVDSLGINEQELTFLSHIANGPHMEEYPVQAGTVHVHKVVM
25 HP LFWILKEHGR-----SKSRASDLTRIHFHTLVYHILATVDGHWANQLAAVAAGARVAGT
* * . . . * . . . * . . . * . . . . . * . . . . . * . . . . .
CE LHWLLKTYGRDPTGQIASKTGYRLSRIHFHCLTYHIMVSSGTDWSNLAAGLAAGARIAGR
HP QAC--ATETIDTSRVSLRAPQEFMTSHSEAGSRIVLNPKNKPVVEWHREGISFHFTPVVLC
* . . . . * . . . . . * . . . . .
30 CE LSCNIGANTMDSELLEIRTPANFVLDKKIEKNYQFEAHKYMLTPFNIRACSTRLLIRRKPP
HP KDPIRTVGLGDAISAEGLFYSEVHPHY
CE GGGILDEGVTFSDVHNVLNPTTRLPYPEEQLEHIEKTSSEIMKERNKIRYGTRKKKDS

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356000) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10628> (SEQ ID NOS: 63, 73, and 83)

10 Determination of the whole base sequence of the cDNA insert of clone HP10628 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 66-bp 5'-untranslated region, a 1254-bp ORF, and a 297-bp 3'-untranslated region. The ORF encodes a
15 protein consisting of 417 amino acid residues and there existed four putative transmembrane domains. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
20 product of 46 kDa that was almost identical with the molecular weight of 45,461 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schistosoma mansoni* ATP-cassette
25 family protein (GenBank Accession No. L26286). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Schistosoma mansoni* ATP-cassette family protein (SM). Therein, the marks of -, *, and . represent a gap, an amino
30 acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

both proteins shared a homology of 39.5% in the C-terminal region of 294 amino acid residues.

Table 17

5	HP MLVHLFRVGIRGGPFPGRIPLPLRFQTFSAVRYSDGYRSSSLRAVAHLRSQWHLPRAS SM MFSALCRRGFLTNKVSQFRSTYKCDHYNLKT
	HP PLAPRWSPSAWCWVGALLGPMVLSKHPHLCVALCEAEEAPPASSTPHVVGSRFNWKLF SM HIKPLKCSSLRLTVGTGLFIALHISKISPESRIQTVQCEVDSYQTDQITFAKSGGIPRYI
10	HP WQFLHPHLLVLGVAVVLALGAALVNVQIPLLLGQLEVVAKYTRDHVGSFMTESQNLSTH .. *. . * .. *. ***** ** ..* * * .. . SM GVLILPDCVYLFGAILGAFVAAMNVYIPLYLGDFVSSLSRCVVTHEG-FVSAVYVPTLR HP LLILYGVQGLLTFGYLVLLSHVGERMAVDMRRALFSSLLRYCQPOGAELGQDITFFDANK * * .*. * * *. ** .***** ** .**..* * *****
15	SM LCSSYLLQSLSTFLYIGLLGSVGERMARRMRIQLFRKLV-Y-----QDVAYFDVHS HP TGQLVSRLTTDVQEFKSSFKLVISQGLRSCQVAGCLVLSMLSTRLLLMVATPALMG ..***.***** *****. .**.*.. * .*. ** * . * .. SM SGKLVEIIGSDVQNFKSSFQKQCISQGLRNGIQVVGSVFALLSISPTLTAALIGCLPCVFL HP VGTLMGSLRKLSQCQCEQIARAMGVADALGNVRTVRAFAMEQREEERYGAEEACRCR 20 ..*****.***. . *. * . . .*****. SM IGSLMGTELRLHISREVQSQNSLFASLIDEAFSHIRTVKSLAMEDFLINKINYNDKAKML HP AEELGRGIALFQGLSNIAFNCMVLGTLFIGGSLVAGQQLTGGLMSFLVASQTVQRL ..*. *. *****..* .***.*..* *.. .**.*.*****.....** SM SEKLSFGIGSFQGLSNLTNGVVLGVLYVGHLMSRGELDAGHLMSFLATTQTLQSLTQ
25	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. U66688) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10629> (SEQ ID NOS: 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10629 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure
5 consisting of a 259-bp 5'-untranslated region, a 1950-bp ORF, and a 1060-bp 3'-untranslated region. The ORF encodes a protein consisting of 649 amino acid residues and there existed at least eight putative transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile,
10 obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
15 protein was similar to the *Caenorhabditis elegans* hypothetical protein CELF38B6 (GenBank Accession No. U40060). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELF38B6 (CE).
20 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.1% in the C-terminal
25 region of 445 amino acid residues.

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA450191) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10635> (SEQ ID NOS: 65, 75, and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10635 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 65-bp 5'-untranslated region, a 282-bp ORF, and a 111-bp 3'-untranslated region. The ORF encodes a protein consisting of 93 amino acid residues and there existed two putative transmembrane domains. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 9,489 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA516481) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10636> (SEQ ID NOS: 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10636 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 179-bp 5'-untranslated region, a 1278-bp ORF, and a 255-bp 3'-untranslated region. The ORF encodes a protein consisting of 425 amino acid residues and there existed ten putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43270) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10640> (SEQ ID NOS: 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10640 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 52-bp 5'-untranslated region, a 450-bp ORF, and a 553-bp 3'-untranslated region. The ORF encodes a protein consisting of 149 amino acid residues and there existed at least two putative transmembrane domains. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was almost identical with the molecular weight of 16,829 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical

protein F27F23.14 (GenBank Accession No. AC003058). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Arabidopsis thaliana hypothetical protein F27F23.14 (AT).
 5 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire
 10 region other than the N-terminal region.

Table 19

	HP	METLYRVPFLVLECPNLKCLKPPWLHMPSTMTVYA
15		*** * *.*** * . . .***.*****
	AT	MAPRSDSQTGSSVSDGSDQSSMDPIFHLRIVPFSFLRPPRLRLKIPS-FTLPSPMTVYA
	HP	LVVVSIFLITGGIYDVIVEPPSVGSMTD-EHGHQRPVAFLAYRVNGQYIMEGLASSFLF
	*.....*.....*.....*.....*.....*.....*.....*
	AT	LILLTYFLVVGSGFVYDVIVEPPGIGSTQDPTTGTIRPVVFMSSGRVNGQYIIEGLSSGFMF
20	HP	TMGGLGFIILDRSNAPNIPKLNRFLLFFIGFVCVLLSFFMARVFMRMKLPGYLMG
		..**.*.....*.....*.....*.....*.....*.....*.....*.....*
	AT	VLGGIGIVMLDLALDKNKAKSVKASYAVAGVSSIVIAVMSMLFIRIKIPGYLY

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N34717) among ESTs. However, since
 30 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10644> (SEQ ID NOS: 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10644 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 221-bp 5'-untranslated region, a
5 1191-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 396 amino acid residues and there existed two putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

10 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein B0511.8 (GenBank Accession No. AF067608). Table 20 shows the comparison between amino acid
15 sequences of the human protein of the present invention (HS) and the *Caenorhabditis elegans* hypothetical protein B0511.8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
20 of the protein of the present invention, respectively. The both proteins shared a homology of 31.3% in the region of 361 amino acid residues other than the N-terminal region and the C-terminal region.

Table 20

HS	MAMIELGFGRQNFHPLKRKSSLLKL
CE	CDKNGQYLSVQEEIDAENKVQRKIAPGLNEKVLERVQTQMLMKQEKSTETYMIWLKNLRVP
5	HS IAVVFAVLLFCEFLIYYLAIFQCNWPEVKTTASDGEQTTREPVLKAMFLADTHLLGEFLG
	* * * * * * *
CE	ILLAILLVYNEYFIFFIASFSCQWP-----CKYGRCS-ESSVKAFMISDTHLLGKING
HS	HWLDKLRREWQMERAFQTALWLLQPEVVFILGDIFDEGKWSTPEAWADDVERFQKMFRHP
	***** * * * * *
10	CE HWLDKLRREWQMYQSFWISTWIHSPDVTFFLGDLMDEGKWAGRPFVEAYAERFKKLF--G
HS	SHVQLKVAGNHDIGFHYEMNTYKVERFEKVFSSERLFSWKGINFVMVNSVALNGDGCGI
 * * * * *
CE	DNEKVITLAGNHDLGPHYAL----VQTFATHLTPT--VELKNYLLIMPETLEMFKKEFR
HS	CSETEAELIEVSHRLNCSREARG-SSR-CGPGPL-----LPTSAPVLLQHYPLYRRS
15	* * * * * * *
CE	GLIDEMKIKKHRFVLINSMAMHGDGCRLCHEAELILEKIKSRNPKNRPVLQHFPLYRKS
HS	DANCSGEDAAPAEERDIPFKENYDVLVSREASQKLLWWLQPRVLVSGHTHSAC-----EVH
	* * * * * *
CE	DAECDQVDEQHEIDLKEMYREQWDTLSKESSLQIIDS LNPKAVFGGHTHKMCKKKWNKTG
20	HS HGGRVPELSVPSFSWRNRNPNPSFIMGSITPTDYTL SKCYLPREDVVLIIYC-GVVGFLV
	. . . * . * * * * *
CE	NSEYFYEYTVNSFSWRNGDVPAMLLVVIDGDNVLVSSCRLPSEILQIMVYIFGGIGILAK
HS	LTLTHFGLLASPFLSGLNLLGKRKTR
25	CE MYNDLITPAPLEWNVNNAIVCTAILVMIINVVALIFTIFWCLRSKDEGGEIDSNQGVIN

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R88381) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10656> (SEQ ID NOS: 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10656 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 68-bp 5'-untranslated region, a 1053-bp ORF, and a 739-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was almost identical with the molecular weight of 40,043 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Cys-Thr at position 148, Asn-Tyr-Thr at position 155, Asn-Gln-Thr at position 162 and Asn-Lys-Ser at position 190).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA917816) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10672> (SEQ ID NOS: 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10672 obtained from cDNA library of the

human thymus revealed the structure consisting of a 244-bp 5'-untranslated region, a 462-bp ORF, and a 77-bp 3'-untranslated region. The ORF encodes a protein consisting of 153 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. When expressed in COS cells, a product of 17 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N48700) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03194> (SEQ ID NOS: 91, 101, and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03194 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 120-bp 5'-untranslated region, a 912-bp ORF, and a 2406-bp 3'-untranslated region. The ORF encodes a protein consisting of 303 amino acid residues and there existed four putative transmembrane domains. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the mouse hyperpolarization-activated cation channel HAC3 (GenBank Accession No. AJ225124). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the mouse hyperpolarization-activated cation channel HAC3 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 92.5% in the N-terminal region of 293 amino acid residues.

Table 21

15	HS	MEAEQRPAAGASEGATPGLEAVPPVAPPPATAASGPIPKSGPEPKRRHLGTLTLLQPTVNKF
		.**.*.***. *. **.*..* ***** .*.*****.*****
	MM	MEEEARPAAGAGEAATPARET-PPAAPAQARAASGGVPESAPEPKRRQLGTLTLLQPTVNKF
	HS	SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE

20	MM	SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE
	HS	ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS

	MM	ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS
	HS	IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHWEEIFHM
25		*****
	MM	IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHWEEIFHM
	HS	TYDLASAVVRIFNLIQMMLLLCHWDGCLQFLVPMLQDFPPDCWVSINHMVVRSPHSSAFP
		*****.*****.*.***.*
	MM	TYDLASAVVRIFNLIQMMLLLCHWDGCLQFLVPMLQDFPPDCWVSMNRMVNHWSGRQYSH
30	HS	GPS
	MM	ALFKAMSHMLCIGYGQAPVGMPPDVWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRQY

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI571225) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03219> (SEQ ID NOS: 92, 102, and 112)

10 Determination of the whole base sequence of the cDNA insert of clone HP03219 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 55-bp 5'-untranslated region, a 852-bp ORF, and a 237-bp 3'-untranslated region. The ORF encodes a protein consisting
15 of 283 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
20 of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human putative membrane protein 54Tm (GenBank Accession No. AF004876). Table 22 shows the
25 comparison between amino acid sequences of the human protein of the present invention (HS) and the human putative membrane protein 54Tm (TM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino
30 acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 56.5% in the entire region.

Table 22

20

25

<HP03236> (SEQ ID NOS: 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP03236 obtained from cDNA library of human

fibrosarcoma cell line HT-1080 revealed the structure consisting of a 252-bp 5'-untranslated region, a 1467-bp ORF, and a 620-bp 3'-untranslated region. The ORF encodes a protein consisting of 488 amino acid residues and there
5 existed seven putative transmembrane domains. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

10 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein ZC513.5 (GenBank Accession No. U53155). Table 23 shows the comparison between amino acid sequences
15 of the human protein of the present invention (HS) and the *Caenorhabditis elegans* hypothetical protein ZC513.5 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
20 of the protein of the present invention, respectively. The both proteins shared a homology of 39.5% in the intermediate region of 365 amino acid residues.

Table 23

```

HS  MAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQATHDLLYHWQDLEQYDHLEF
                                     .*** .*
5  CE                                     MKMKYDHSQF
HS  PGVVPRTFLGPVVIADVSSPAVYVLSLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRR
    *****.*. .*.*** ..... *..*..*** ... ..*.*
CE  PGVVPRTFIGPISLAILSSPMSFIFRFWAIPKMWQLLIRATLGLMNAMAFLYFARSVNR
HS  HFGAMVATMFCWVTAMQFHLMFYCTRTPNVLALPVLLALAAWLREHARFIWLSAFAI
10  **. * . . *** .** .*.***.*** .*.*** * ... ..
CE  KFGRETAMYLRLIMCTQFHYIFYMSRPLPNTFALILVMIVFERLLEGRYESAVRYATASV
HS  IVFRVELCLFLGLLLL--LALGNRKV-SVVRALRHAVPAGILCLGLTVAVDSYFWRQLTW
    *.** ** *. * ..* . *. ** . *. *. . .***.....***** . *
CE  ILFRCELVLVLYGPIFLGYMISGRLLKVFGEFGAIAIGVRIAAMCLAVSIPIDSYFWRPLW
15  HS  PEGKVLWYNTVLNKSSNWGTSPILWYFYSALPRGLGCSLLFIPLG-LVDRRTHAPTVAL
    ***.*...*. *.* ....*.***** * .*.*** ***** .. ...
CE  PEGEVMMFFNVVENRSHEYGTQFPLWYFYSALPRCLLTTLVPLGLLVDRRLPQIVLPSV
HS  GFMALYSLLPHKELRFIIYAFPMNLITAARGCSYLLNNYKSWLYKAGSLLVIGHLVNA
    *.***.*****.....*..*** *. *.* ..*.. . ** *.*..
20  CE  IFIFLYSFLPHKELRFIIYVLPFCLSAAVFCARMLINRHKSFFRMILFFGVILHLLANV
HS  AYSATALYVSHFNYPGGVAMQ--RLHQLVPPQTDVLLHIDVAAAQTVSRFLQVNSAWRY
    ... *.*. **** *.. .... ... * ..** * *****.*..*.*
CE  LCTGMFLLVASKNYPGFDALNYLQFQNRFDKPKVTVYIDNACAQTVNRFHINDAWT

```

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA744858) among ESTs. However, since

30 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03237> (SEQ ID NOS: 94, 104, and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03237 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 101-bp 5'-untranslated region, a 549-bp ORF, and a 1106-bp 3'-untranslated region. The ORF encodes a protein consisting of 182 amino acid residues and there existed four putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human intestinal membrane A4 protein (SWISS-PROT Accession No. Q04941). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human intestinal membrane A4 protein (IM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the intermediate region of 111 amino acid residues.

Table 24

```

HS MWPPDPDPDPDPPEAGGSRPGPAVPGLRALLPARAFLCSLKGRIILAEGLSFITFICYV
                                     ** **.* ** *.....*.
5  IM                               MADSERLSAPGCWAACTNFSRTRKGILLFAEIIILCLVILICF-
HS ASSASAFLTAPLLEFLLALYFLFADAMQLNDKWQGLCWPMMDFLRCVTAALYFAISITA
   ..*..... . ...*.....* * . . . . . * . . ** **.* ..*.....* . ....
IM SASTPGYSSLSVIEMILAAIFFVVMCDLHTKIPFINWPWSDFFRTLIAAILYLITSIVV
HS IAKYSDGASKAAGVFGFFATIVFATDFYLIFNDVAKFLKQGDSADETTAHKTEEENSDDSD
10  ... .. . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
IM LVERGNHISKIVAGVLGLIATCLFGYDAYVTFFPVRQPRHTAAPTDPADGPV

```

Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. R14227) among ESTs. However, since
 they are partial sequences, it can not be judged whether or
 not they encode the same protein as the protein of the
 present invention.

<HP03267> (SEQ ID NOS: 95, 105, and 115)

Determination of the whole base sequence of the cDNA
 insert of clone HP03267 obtained from cDNA library of human
 liver revealed the structure consisting of a 148-bp 5'-
 untranslated region, a 555-bp ORF, and a 715-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 184 amino acid residues and there existed two putative
 transmembrane domains. Figure 35 depicts the
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 Doolittle method, of the present protein. In vitro
 translation resulted in formation of a translation product
 of 21 kDa that was almost identical with the molecular

weight of 20,733 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human polyposis locus protein 1 (SWISS-PROT Accession No. Q00765). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human polyposis locus protein 1 (PL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 59.1% in the entire region.

15

Table 25

HS	MDGLRQRVEHFLEQRNLVTEVLGALEAKTGVEKRYLAAGAVTLLSLYLLFGYGASLLCNL
	.*********.....*****,*****
PL	MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFYGASLLCNL
20 HS	IGFVYPAYASIKAIESPskDDDTVWLTYWVYALFGLAEFFSDLLSWFPFYVVGKCAFL
	*** **** *****.*,*** *****.*.....*****.*****.***
PL	IGFGYPAYISIKAIESPnkEDDTQWLTYWVYGVFSIAEFFSDIFLSWFPFYMLKCGFL
HS	LFCMAPRPWNGALMLYQVRVRLFLRHHGAVDRIMNDLSGRALDAAAGITRNVKPSQTPQ
	*.***** * ********.....******
25 PL	LWCMAPSPSNGAELLYKRIIRPFFLKHESQMDSVVKDLKDKSKETADAITKEAKKATVNL
HS	PKDK
	PL LGEEKKST

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. R09702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP03270> (SEQ ID NOS: 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP03270 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 132-bp 5'-untranslated region, a 423-bp ORF, and a 656-bp 3'-untranslated region. The ORF encodes a protein consisting of 140 amino acid residues and there existed four putative transmembrane domains. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was somewhat larger than the molecular weight of 15,864 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein (EMBL Accession No. AL031854). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the *Schizosaccharomyces pombe* hypothetical protein (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.4% in the entire region.

Table 26

```

HS      MSRFLNVLRSWLVMSIIAMGNLTQSFRDHTFLYEKLYTGKPNLVNGLQARTFGI
      ... .* *.***. *. **.*** ... * ...* ...* .....*****
5  SP MSQILAMLPSLIVAKWNVVVSVAALENTVQSFLTPK-LTKRVY-SNTNEVNGLQGRFTGI
HS WTLSSVIRCLCAIDIHNKTLYHITLWTFLLALGHFLSELFVYGTAAPTIGVLAPLMVAS
      *****...* ** .* * ... . *. ** ***** ... *.. . *.***...*..
SP WTLSSAIVRFYCAYHITNPDVYFLCQCTYYLACFHFLEWLLFRRTNLGPGLLSPIVVST
HS FSILGMLVGLRYLEVEPVSRQKRN
10      **
SP VSIWFMAKEKASILGIAA

```

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T30721) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
20 present invention.

<HP03298> (SEQ ID NOS: 97, 107, and 117)

Determination of the whole base sequence of the cDNA insert of clone HP03298 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 182-bp 5'-untranslated region, a 462-bp ORF, and a 455-bp 3'-untranslated region. The ORF encodes a protein consisting of 153 amino acid residues and there existed at least one putative transmembrane domain. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17.5 kDa that was almost identical with the molecular

weight of 17,360 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein SPBC119.09c (EMBL Accession No. AL022117). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the *Schizosaccharomyces pombe* hypothetical protein SPBC119.09c (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.9% in the entire region other than the N-terminal region.

Table 27

HS	MNVGVAHSEVNPNTVMNSRGMWLTALGVGLLHIVLL
20	. * . * * * . . .
SP	MGSSSSRRSSSLVTKVPKPTIDDRLDQGSATNYSNWNVNYKGAWVIHIVLIAALRLIFH
HS	SIPFFSVPAWTLTNIHNLGMYVFLHAVKGTFFETPDQ GKARLLTHWEQLDYGVOFTSS
	. ** * . ***** . . . * . . . * . . . * . . . * . . .
SP	AIPSVSRELAWTLTNLT YMAGSFIMFHWVTGTPFEFNGGAYDR-LTMWEQLDEGNQYTPA
25	HS RKFFTISPIILYFLASFYTKYDP THFILNTASLLSVLIPKMPQLHGVRIFGINKY
	** . . ***** ** . . * . . . * . . ***** . . . *
SP	RKYLLVLP IILFLMSTHYTHYNGWMFLVNIWALFMVLIPKLPVHRKRIFGIQKLSLRDD

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA043039) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP10631> (SEQ ID NOS: 98, 108, and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10631 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 226-bp 5'-untranslated region, a
10 522-bp ORF, and a 2741-bp 3'-untranslated region. The ORF encodes a protein consisting of 173 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

15 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W26443) among ESTs. However, since they are partial sequences, it can not be judged whether or
20 not they encode the same protein as the protein of the present invention.

<HP10658> (SEQ ID NOS: 99, 109, and 119)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10658 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 24-bp 5'-untranslated region, a 228-bp ORF, and a 679-bp 3'-untranslated region. The ORF encodes a protein consisting of 75 amino acid residues and there
30 existed two putative transmembrane domains. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 14 kDa or less that was almost identical with the molecular weight of 8,625 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T85006) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10663> (SEQ ID NOS: 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10663 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 67-bp 5'-untranslated region, a 480-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 159 amino acid residues and there existed two putative transmembrane domains. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA336522) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03165> (SEQ ID NOS: 121, 131, and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03165 obtained from cDNA library of human

epidermoid carcinoma cell line KB revealed the structure consisting of a 128-bp 5'-untranslated region, a 1911-bp ORF, and a 1195-bp 3'-untranslated region. The ORF encodes a protein consisting of 636 amino acid residues and there
5 existed a putative secretory signal at the N-terminus. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was smaller than the
10 molecular weight of 72,033 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 33.

15 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human β -galactosidase (GenBank Protein ID No. AAA51822). Table 28 shows the comparison between amino acid sequences of the human protein of the
20 present invention (HP) and the human β -galactosidase (GL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The
25 both proteins shared a homology of 37.8% in the entire region.

BNSDOCID: <WO 0029448A2 I >

HP RNQYIK

GL FVDRPVIGSSVTYDHPSKPVEKRLMPPPPQKNKDSWLDHV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA054017) among ESTs. However, since
10 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03266> (SEQ ID NOS: 122, 132, and 142)

15

Determination of the whole base sequence of the cDNA insert of clone HP03266 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 69-bp 5'-untranslated region, a 957-bp ORF, and a 1464-bp 3'-untranslated region. The ORF encodes a
20 protein consisting of 318 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a
25 translation product of 34 kDa that was almost identical with the molecular weight of 35,363 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana putative
30 ribitol dehydrogenase (GenBank Protein ID No. AAC23625). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the

Arabidopsis thaliana putative ribitol dehydrogenase (AT).
 Therein, the marks of -, *, and . represent a gap, an amino
 acid residue identical with that of the protein of the
 present invention, and an amino acid residue similar to that
 5 of the protein of the present invention, respectively. The
 both proteins shared a homology of 39.0% in the region of
 483 residues other than the N-terminal region.

Table 29

10

HP MVELMFPLLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE

* * * *

AT MGIYGVMTGKKGKSGFGSASTAEDVTQAI DASHLTAIITGGTSGIGLEAARV

HP LAQRGARVYLACRDVEKGELVAKEIQTTTGNQQVLVRKLDLSDTKSIRAFAGFLAEKHX

15

** *** . * * * * * *

AT LAMRGAVHIIAARNPKAANESKEMILQMNPNARVDYLQIDVSSIKSVRSFVDQFLALNVP

HP LHVLINNAGVMMCPYSKTADGFEMHIGVNH LGHFLLTHLLEKLK-----ESAPSRIVNV

* * * * * *

AT LNILINNAGVMFCPFKLTEDGIESQFATNHIGHFLLTNLLLDKMKSTARESGVQGRIVNL

20

HP SSLAH---HLGRIHFHNLOGEKFYNAGLAYCHSKLANILFTQELARRLKSG--VTTYSV

** . . . * * * * *

AT SSIAHTYTYSEGIKFQGINDPAGYSERRAYGQSKLSNLLHSNALSRRLOEEGVNITINSV

HP HPGTVQSELVRHSSFMRRWWLFSF-FIKTPQOGAQTSLHCALTEGLEILSGNHFSDCHV

*** * . . * . . * * * *

25

AT HPGLVTTNLFYSGFSMKVFRAMTFLFWKNIPQGAATTCYVALHPDLEGVTGKYFGDCNI

HP AWVSAQARNETIARRLWDVSCDLLGLPID

. * * * . . * * *

AT VAPSKFATNNSLADKLWDFSVFLIDSISK

30

Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. D17020) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP03287> (SEQ ID NOS: 123, 133, and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03287 obtained from cDNA library of human thymus revealed the structure consisting of a 83-bp 5'-untranslated region, a 249-bp ORF, and a 1133-bp 3'-untranslated region. The ORF encodes a protein consisting of 82 amino acid residues and there existed one putative transmembrane domain at the N-terminus and one at the C-terminus, respectively. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Schizosaccharomyces pombe hypothetical protein 9.0kDa (SWISS-PROT Accession No. 013825). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Schizosaccharomyces pombe hypothetical protein 9.0kDa (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 45.7% in the entire region.

Table 30

```

HP  MAFTLYSLLQAALLCVNAIAVLHEERFLKNIGWGTDOGIGGGFGE-EPGIKSQLMNLI RSV
    *.. ..* ..** ..**.* *..** ..**.. ..**.. ..**..**..**..
5  SP  MFGFGNILYVTL LLLNAVAILSEDRFLGRIGWSQSAAL-GFGDRQDTIKSRILHLIRAI
    HP  RTVMRVPLIIVNSIAIV LLLLFG
    ****  *** ..**.* *..*
    SP  RTVMTFPLIAINTIVIVYNLVLG

```

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA853098) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10665> (SEQ ID NOS: 124, 134, and 144)

20 Determination of the whole base sequence of the cDNA insert of clone HP10665 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 744-bp ORF, and a 142-bp 3'-untranslated region. The ORF encodes a

25 protein consisting of 247 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a

30 translation product of 28 kDa that was somewhat larger than the molecular weight of 25,320 predicted from the ORF. In this case, the addition of a microsome led to the formation

of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from aspartic acid at position 26.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA055367) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10669> (SEQ ID NOS: 125, 135, and 145)

 Determination of the whole base sequence of the cDNA
15 insert of clone HP10669 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 73-bp 5'-untranslated region, a 621-bp ORF, and a 612-bp 3'-untranslated region. The ORF encodes a protein consisting of 206 amino acid residues and there
20 existed one putative transmembrane domain. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration
25 of sequences that shared a homology of 90% or more (for example, Accession No. AF086533) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP10670> (SEQ ID NOS: 126, 136, and 146)

 Determination of the whole base sequence of the cDNA

insert of clone HP10670 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 117-bp 5'-untranslated region, a 1299-bp ORF, and a 606-bp 3'-untranslated region. The ORF encodes a
5 protein consisting of 432 amino acid residues and there existed seven putative transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino
10 acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (GenBank Protein ID No. AAB65910). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP)
15 and the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention,
20 respectively. The both proteins shared a homology of 39.6% in the N-terminal region of 376 residues.

Table 31

HP MDARWWAVVVLAAFP SLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGYLLVQYF
. ** . . * *** . . * . *
5 CE MDRSIMPIDSPARDKPPD--ELVWPLRLFLILLGYSTVATPAAILIYYV
HP RRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLA---PRTEAAETTPMW-----QALKL
**... . . *...* . . * * . . *... *
CE RRNRHAFETPYLSIRLLLLRS-FAVGNPEYQLIPTGEKQARKENDSIPQTRAQCINVIILL
HP LFCATGLQVSYLTWGV LQERV MTRS Y-GATATSPGERFTDSQFLVLMNRVLALIVA--GL
10 ** .*.***. . . *****...*. * *****. *.***. . . *
CE LFFFSGIQVTLVAMGV LQERIITRGYRRSDQLEVEDKFGETQFLIFCNRI VALVLSIMIL
HP SCVLCKQPRH GAPMYRYSFASLSNV LSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKL
. ***.* .*. * .*. * .*. * .*. * .*. * .*. * .*. * .*. * .*. *
CE AKDWTKQPPHPVPLYVHSYTSFSNTISSWCQYEALKYVSFPTQTICKASKVVVTMLMGRL
15 HP VSRRSYEHWEYL TATLISIGVSMFLLSSSGPEPRSSPAT--TL SGLILLAGYIAFDSFTSN
*. ** . . *...*.*****... .*. * .*. *...*.*****. **** *
CE VRGORYSWFEY GCGCTIAFGASLFLSSSSSKGAGSTITYTSFSGMILMAGYLLFDAFTLN
HP WQDALFAYK--MSSVQMMFGVNFFSCLFTVGSILLEQ GALLEGTRFMGRHSEFAAHALLS
...*. * .*. *** . . . **...*.* . * .*.**
20 CE WQKALFDTKPKVSKYQMMFGVNFFSAILCAVSLIEQGLWSSIKFGAEHVDFSRDVFLS
HP ICSACQLFIFYTIGQFGAAVFTIIMTLRQAFAILLSCLLYGHTVTTVVGGLGVAVVFAAL
...* **...*. **...*. **...*. **...*. ** *
CE LSGAIGQIFIYSTIERFGPIVFAVIMTIRQIFIRNTLIRAEDHRGVEMAPPPPPPEPFRLK
HP LLRVYARGRLKQRGKKAVPVESPVQKV
25 CE FL SMIIAVIHI

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z46196) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the

present invention.

<HP10671> (SEQ ID NOS: 127, 137, and 147)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10671 obtained from cDNA library of human
thymus revealed the structure consisting of a 74-bp 5'-
untranslated region, a 921-bp ORF, and a 232-bp 3'-
untranslated region. The ORF encodes a protein consisting of
306 amino acid residues and there existed a putative
10 secretory signal at the N-terminus and one putative
transmembrane domain at the intermediate region. Figure 47
depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA357141) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
20 present invention.

<HP10673> (SEQ ID NOS: 128, 138, and 148)

Determination of the whole base sequence of the cDNA
insert of clone HP10673 obtained from cDNA library of the
25 human thymus revealed the structure consisting of a 203-bp
5'-untranslated region, a 1668-bp ORF, and a 339-bp 3'-
untranslated region. The ORF encodes a protein consisting of
555 amino acid residues and there existed one putative
transmembrane domain. Figure 48 depicts the
30 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product

of 65 kDa that was somewhat larger than the molecular weight of 61,781 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R96413) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10

<HP10675> (SEQ ID NOS: 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10675 obtained from cDNA library of the human thymus revealed the structure consisting of a 92-bp 5'-untranslated region, a 753-bp ORF, and a 648-bp 3'-untranslated region. The ORF encodes a protein consisting of 250 amino acid residues and there existed at least one putative transmembrane domain. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356139) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25

<HP10683> (SEQ ID NOS: 130, 140, and 150)

30

Determination of the whole base sequence of the cDNA insert of clone HP10683 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure

consisting of a 25-bp 5'-untranslated region, a 525-bp ORF, and a 714-bp 3'-untranslated region. The ORF encodes a protein consisting of 174 amino acid residues and there existed one putative transmembrane domain. Figure 50 depicts
5 the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 22 kDa that was somewhat larger than the molecular weight of 19,572 predicted from the ORF. In this case, the addition
10 of a microsome led to the formation of a product of 24 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 27).

15 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA482321) among ESTs. However, since they are partial sequences, it can not be judged whether or
20 not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

25 The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the
30 proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents

which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The

desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; 5 Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed 10 herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or 15 that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been 20 partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, 25 of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, 30 preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153;

5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75%

sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the Table 32 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺] + 0.41 (%G+C) · (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing

polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID NOS: 1
5 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA encoding the protein according to
Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID NOS:
10 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and
141 to 150.

5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.

Fig.1

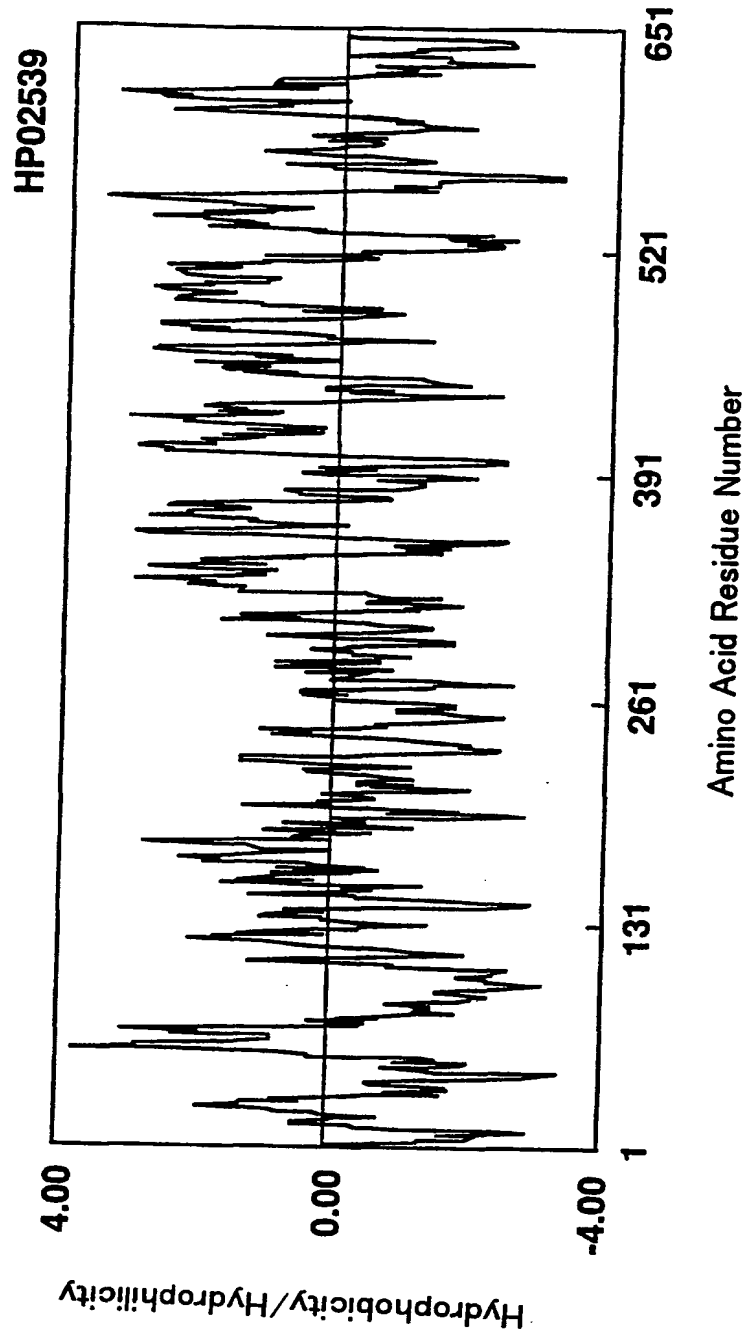
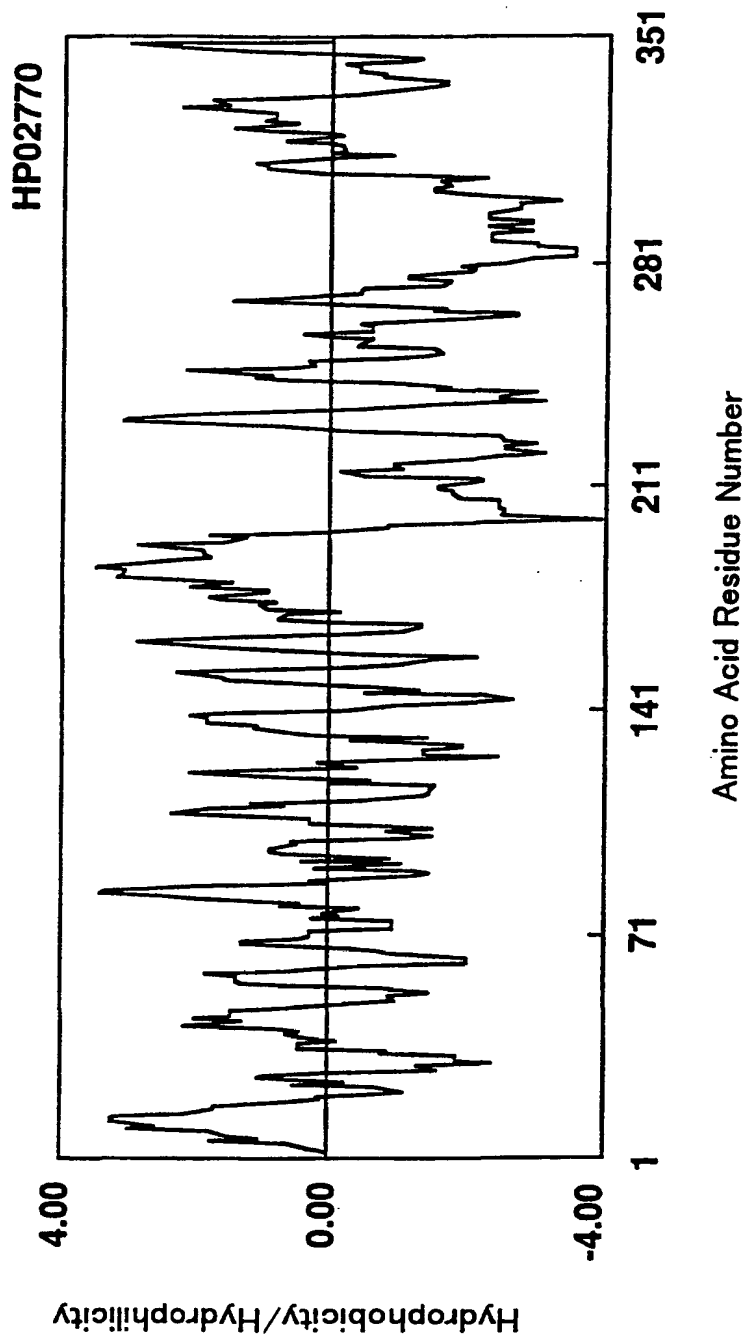
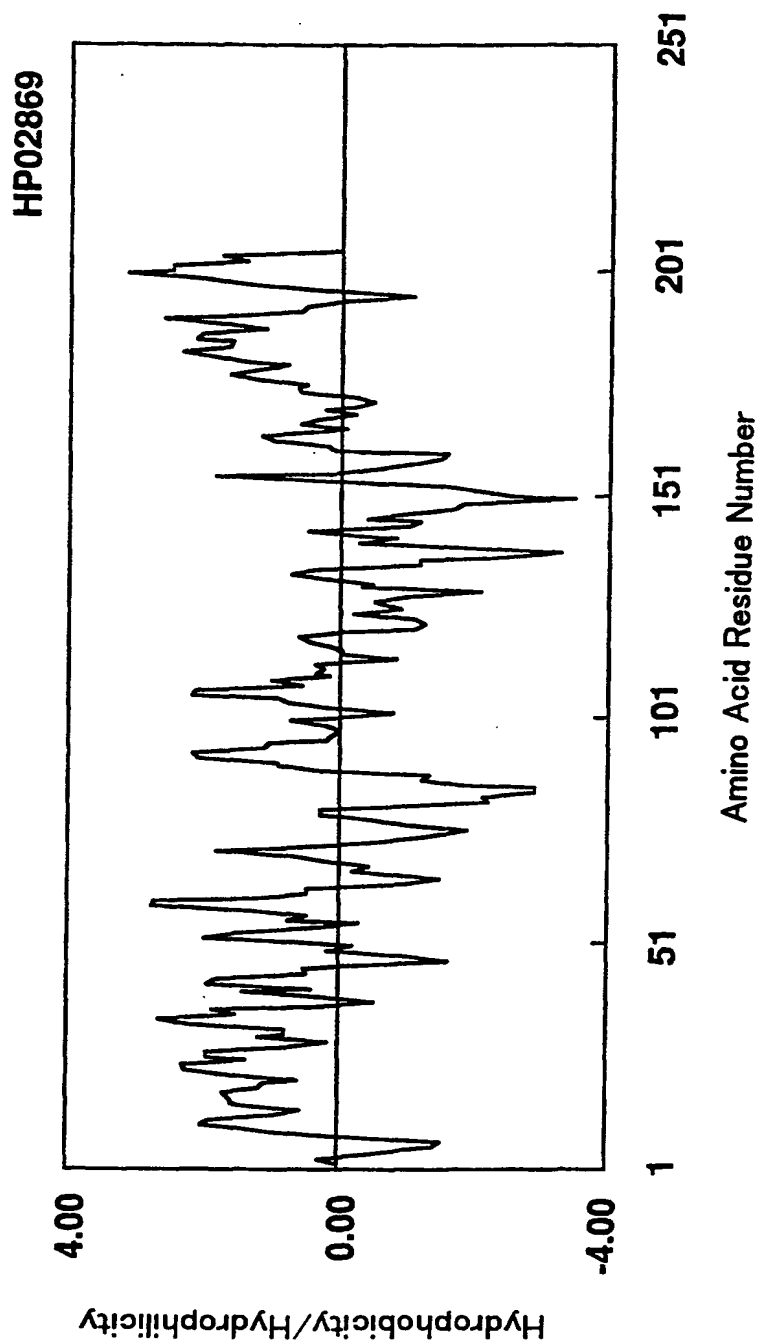


Fig.2



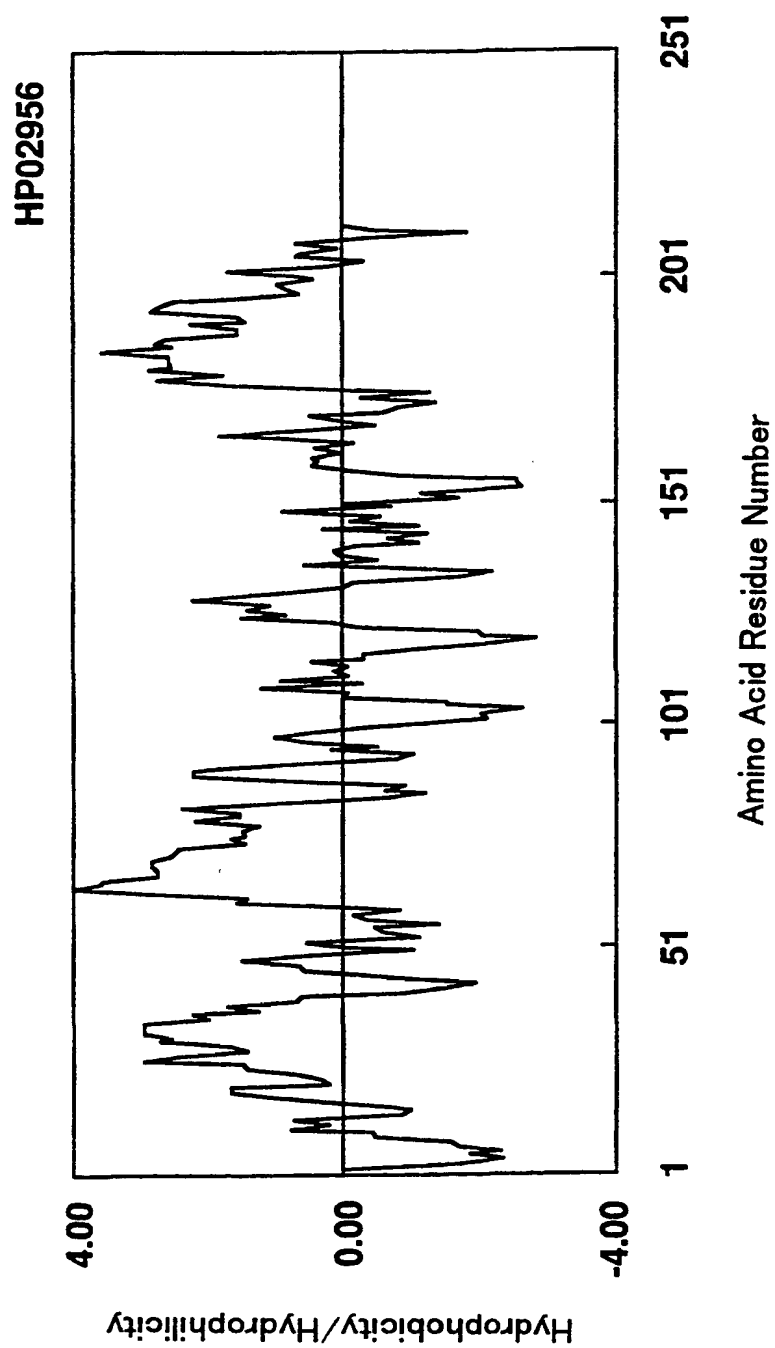
3/50

Fig.3



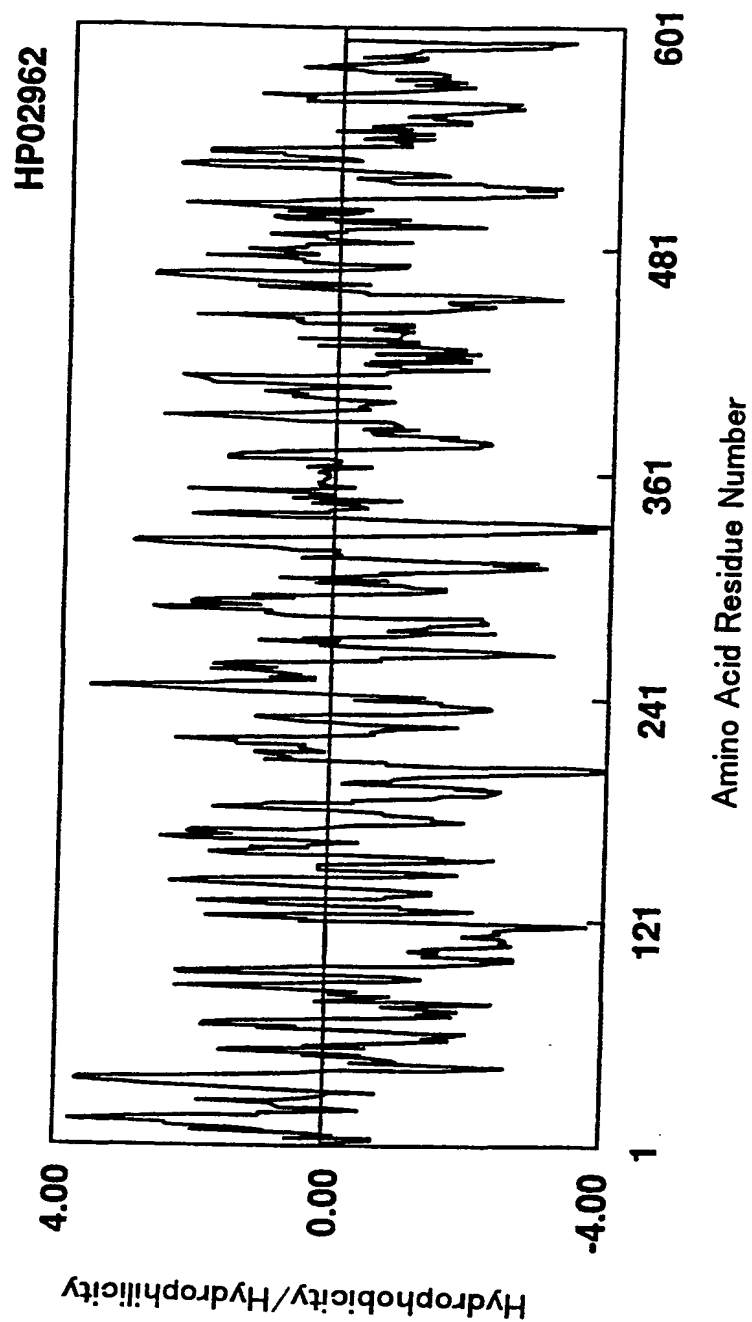
4/50

Fig.4



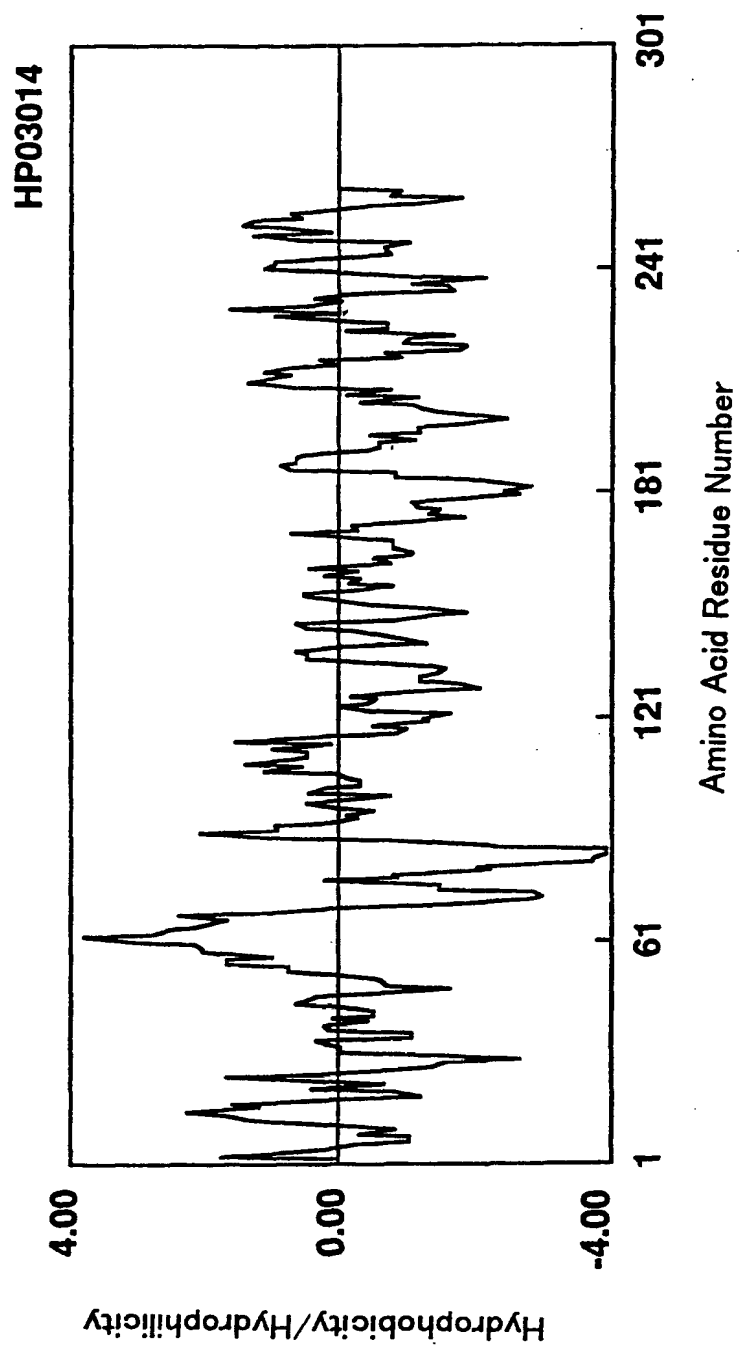
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Fig.5



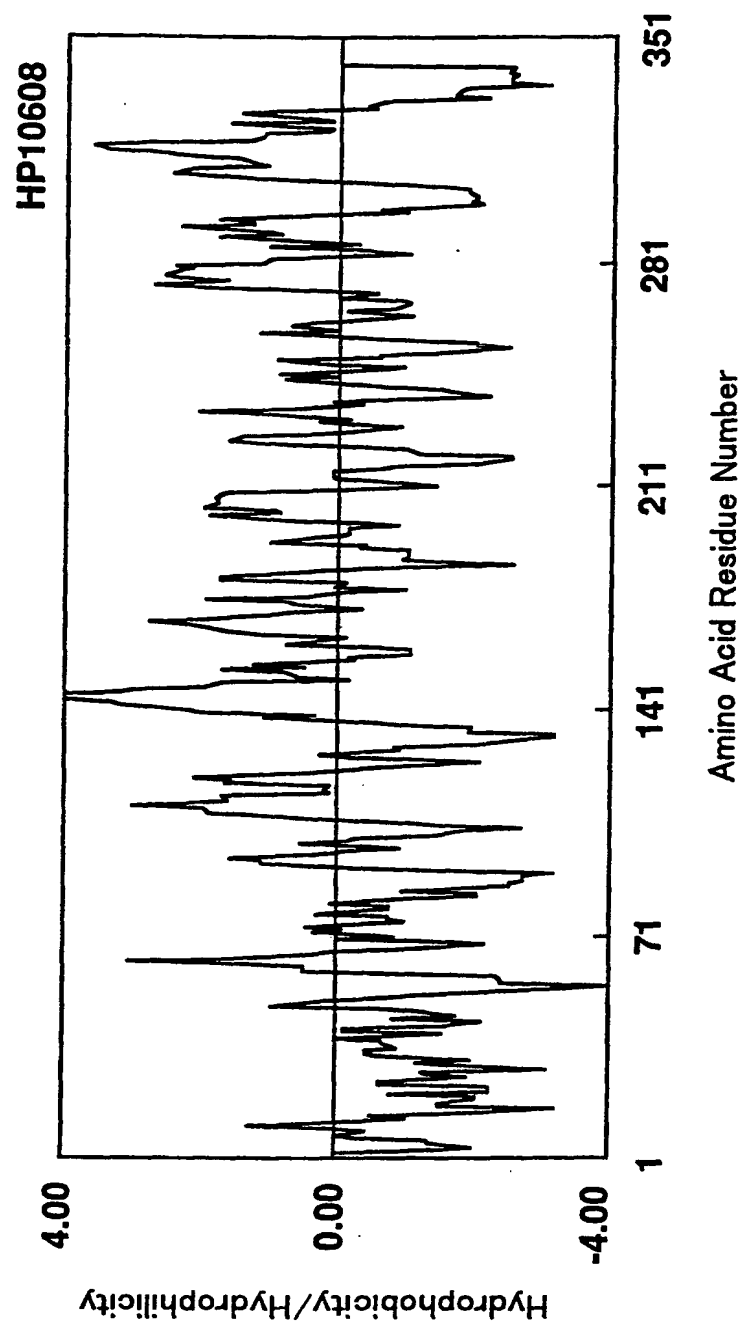
6/50

Fig.6



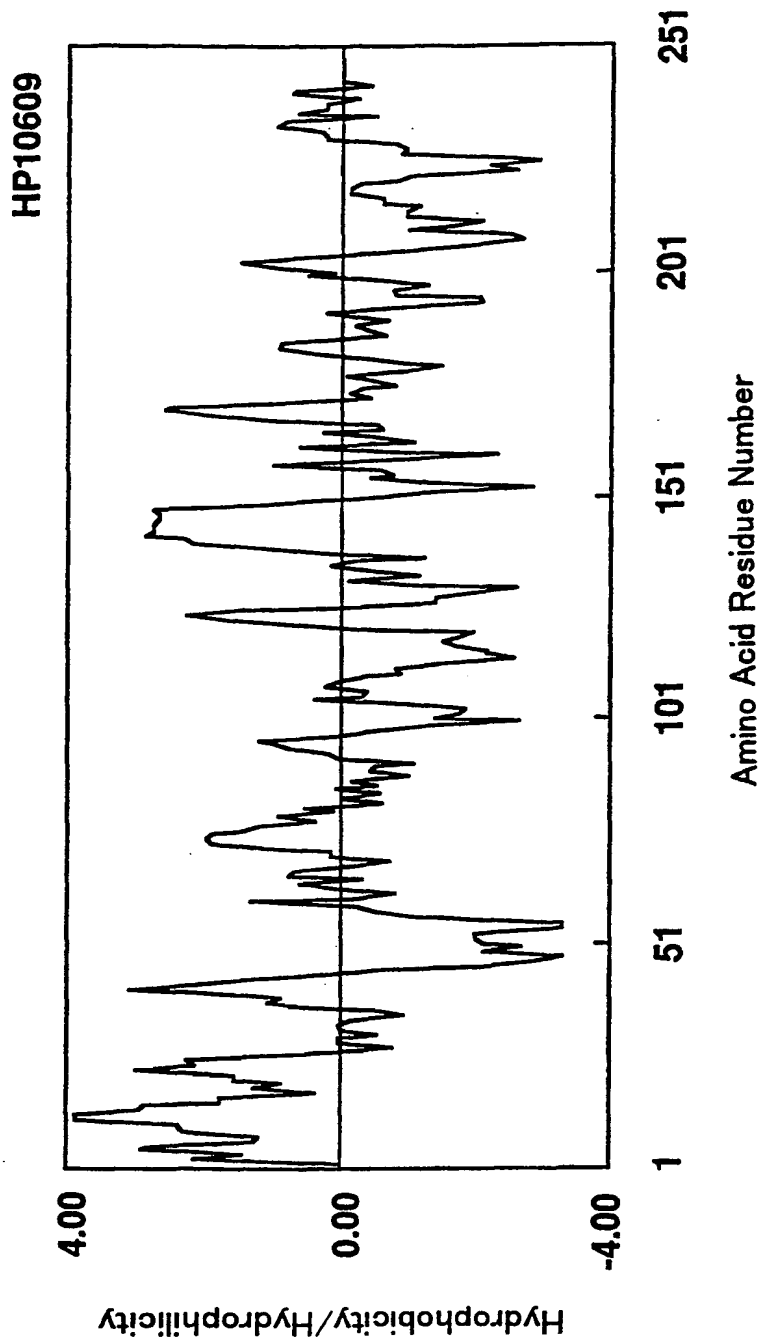
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Fig. 7



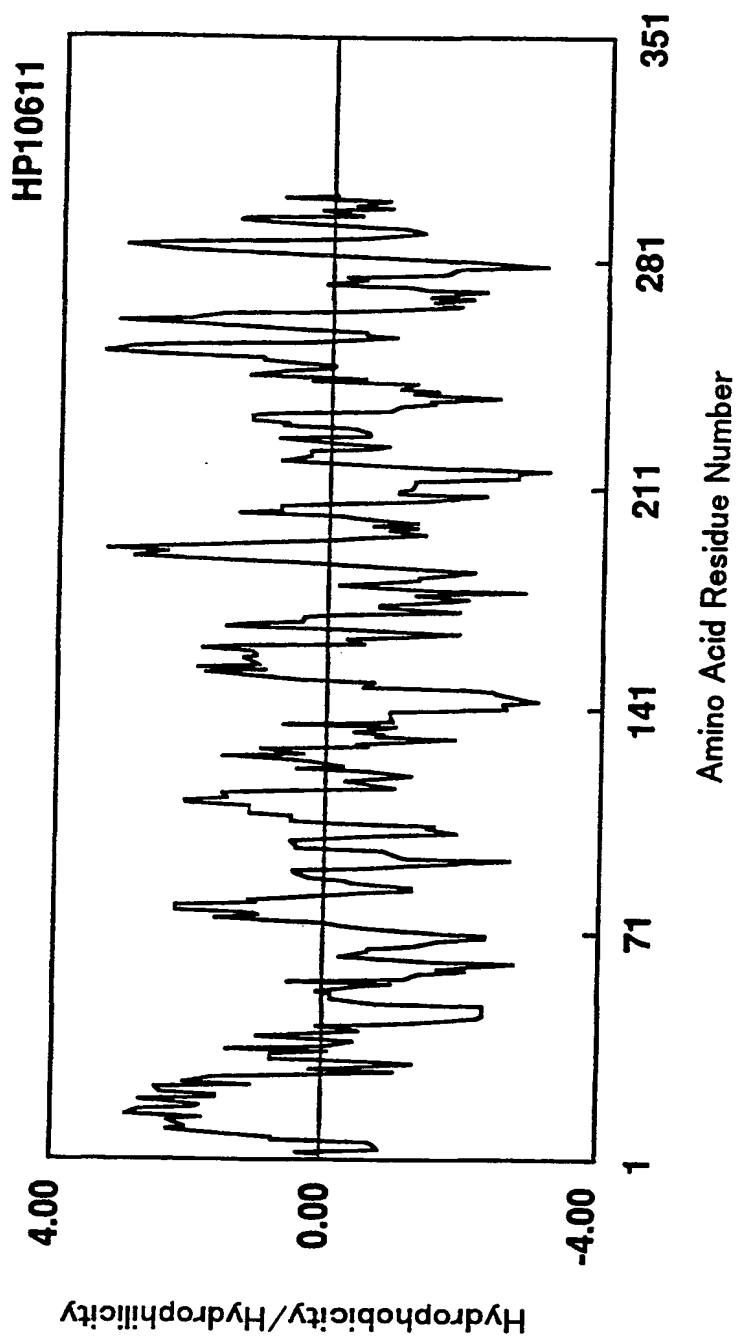
8/50

Fig.8



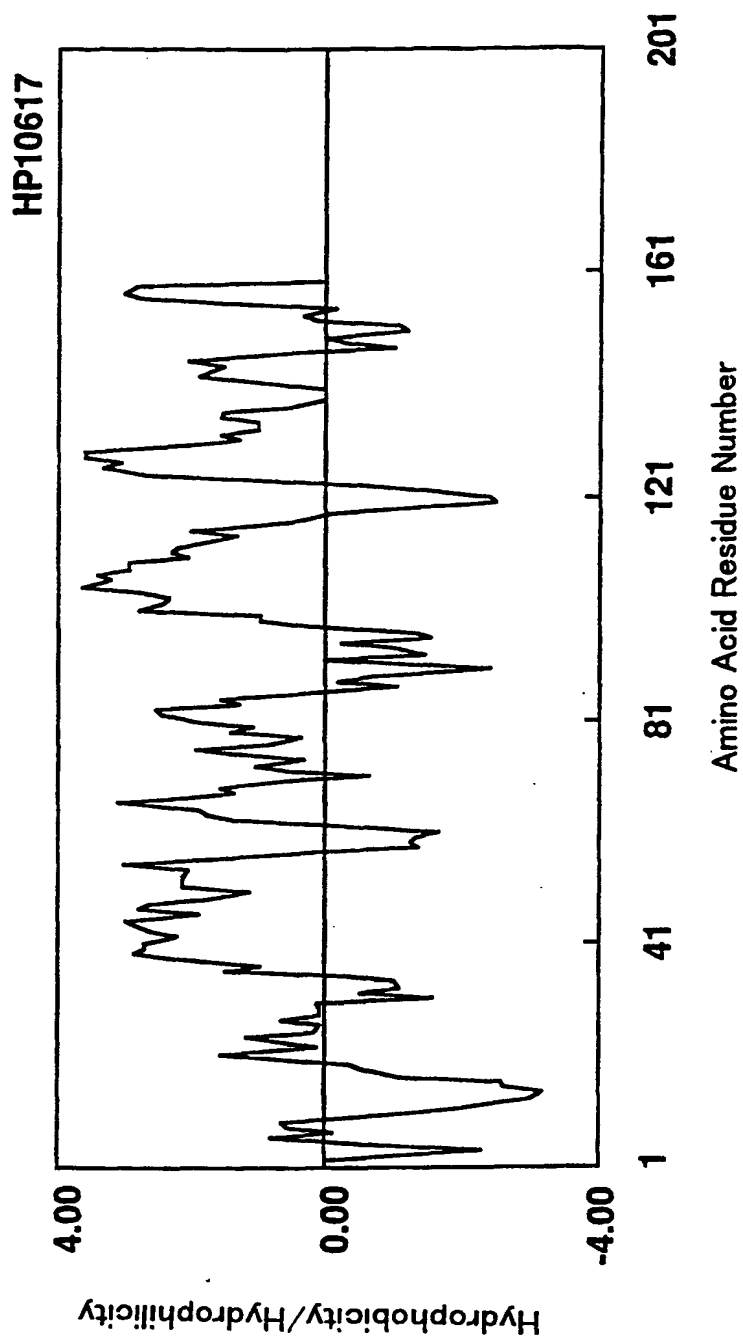
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Fig.9

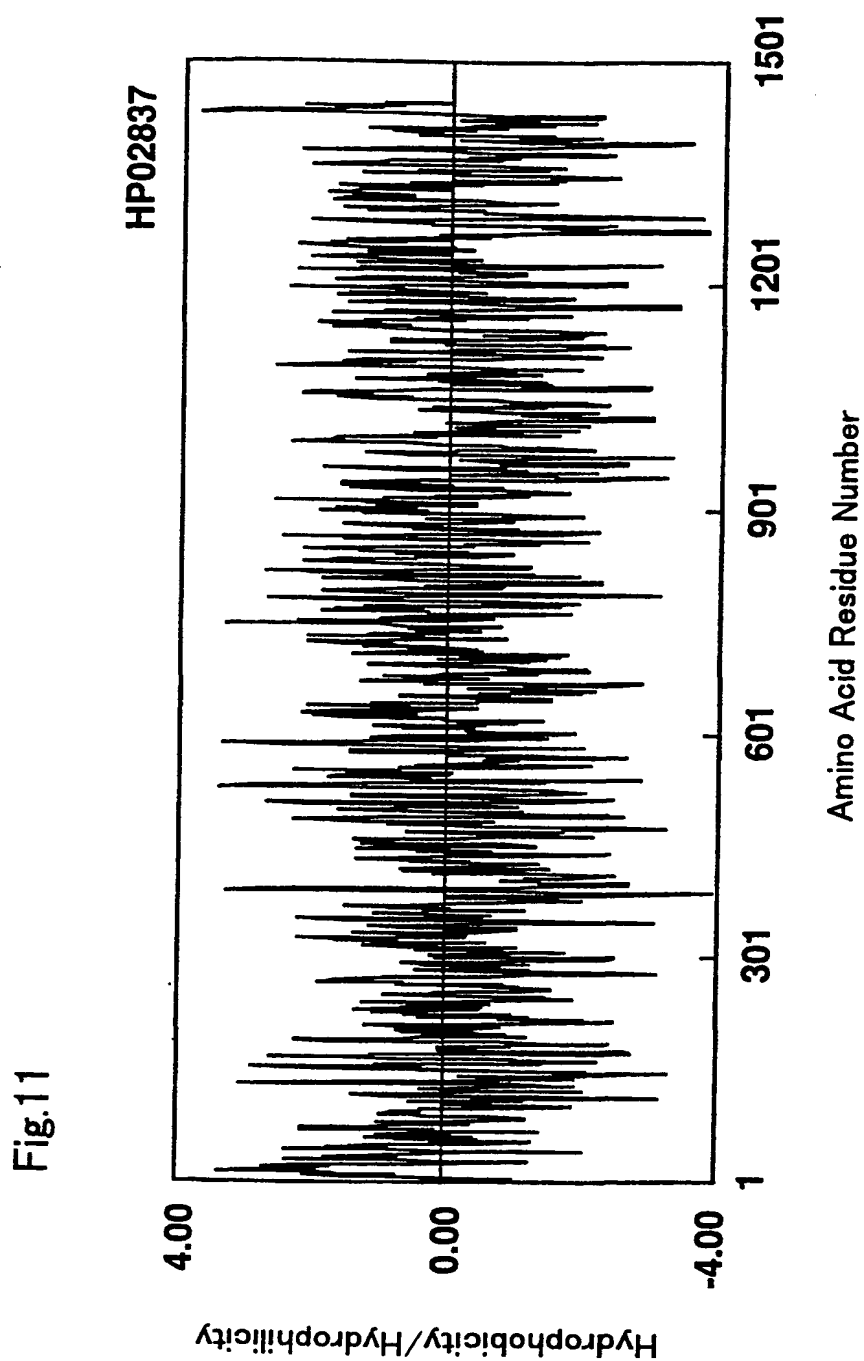


10/50

Fig.10

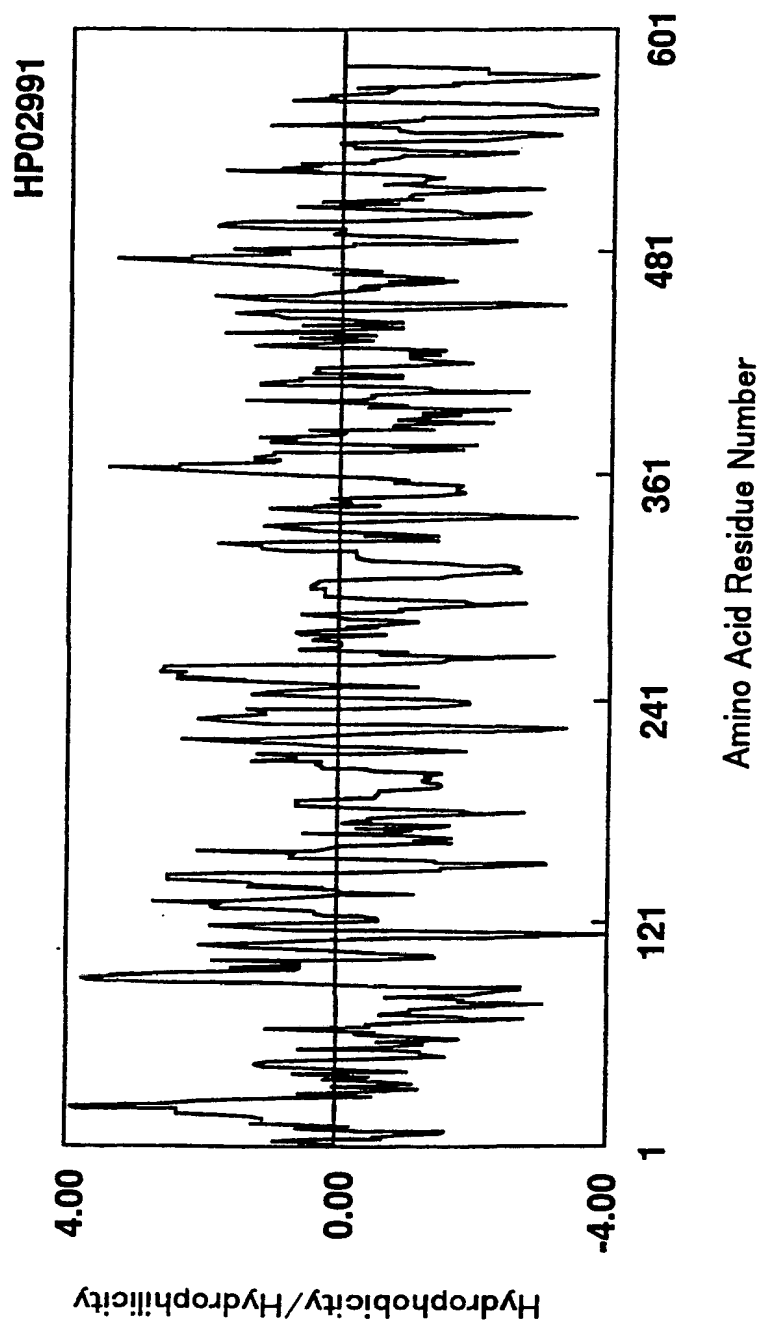


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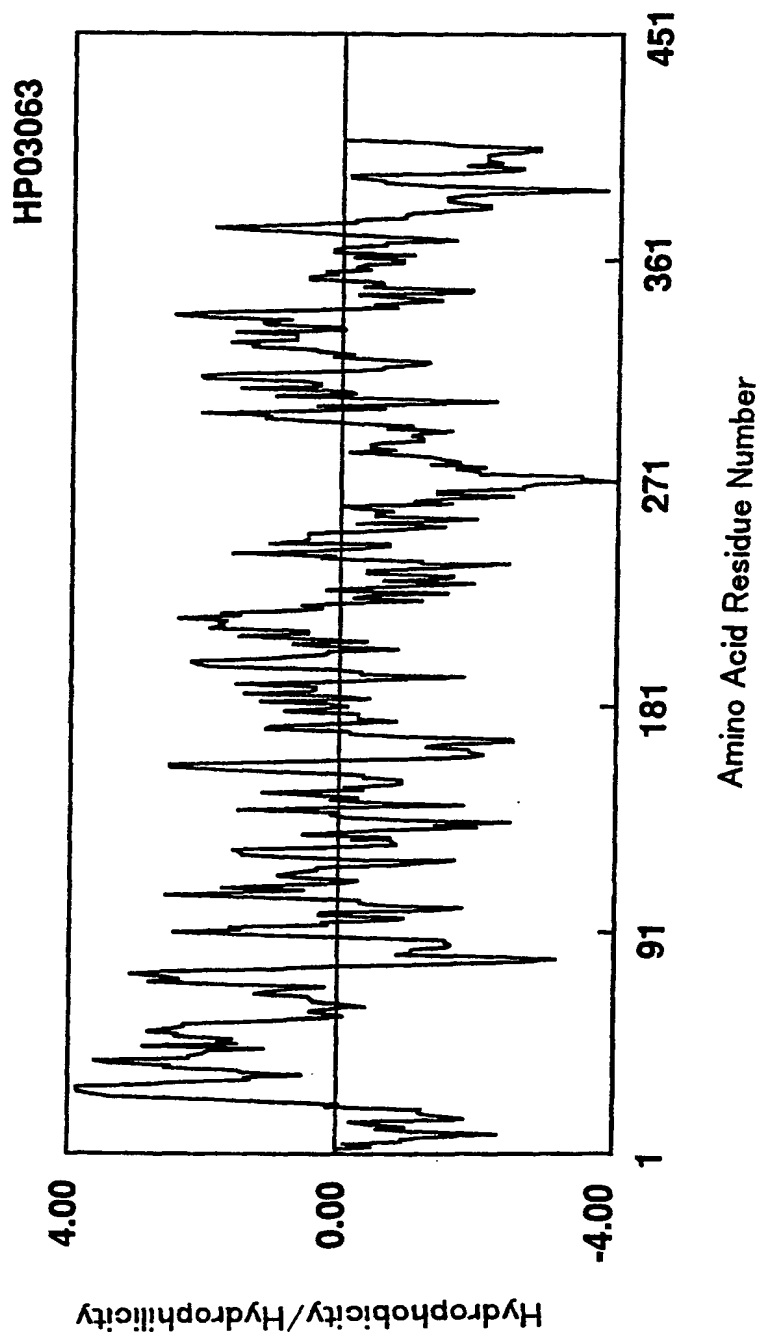
12/50

Fig.12



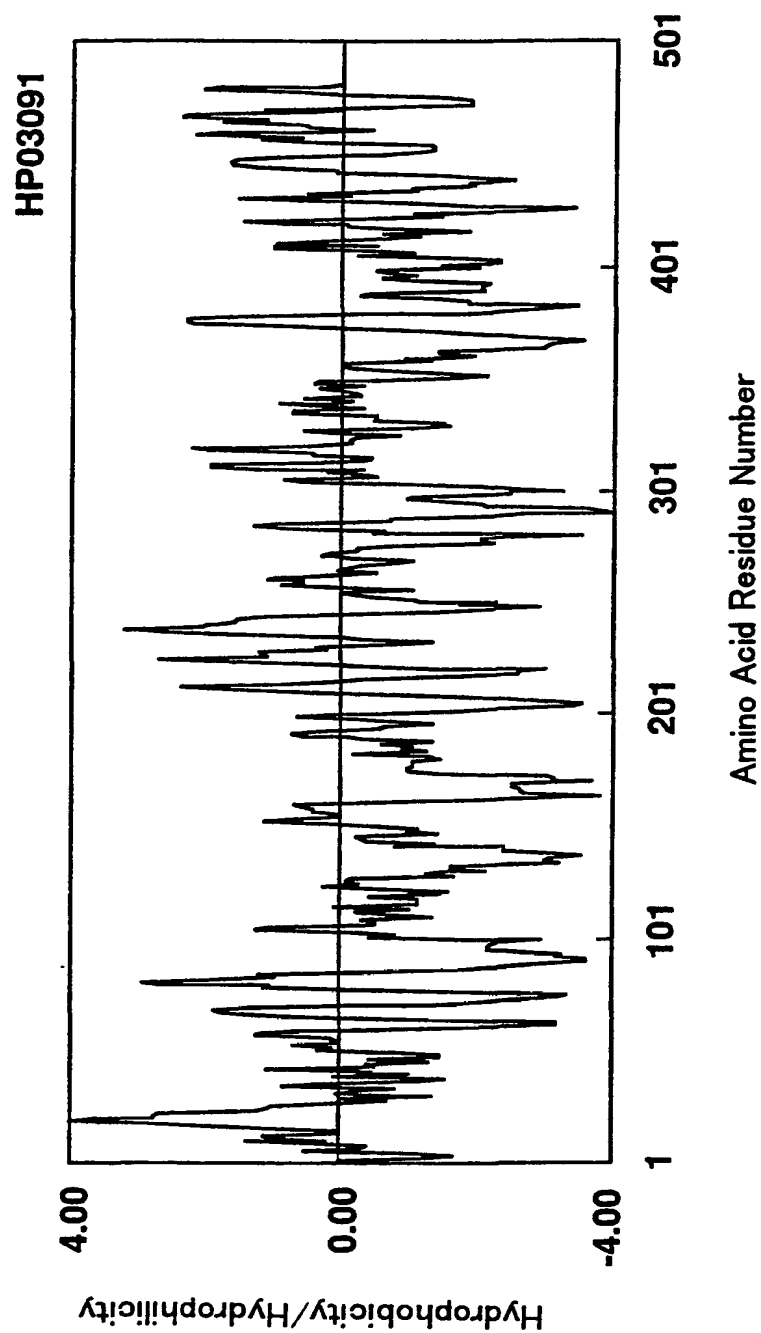
13/50

Fig.13



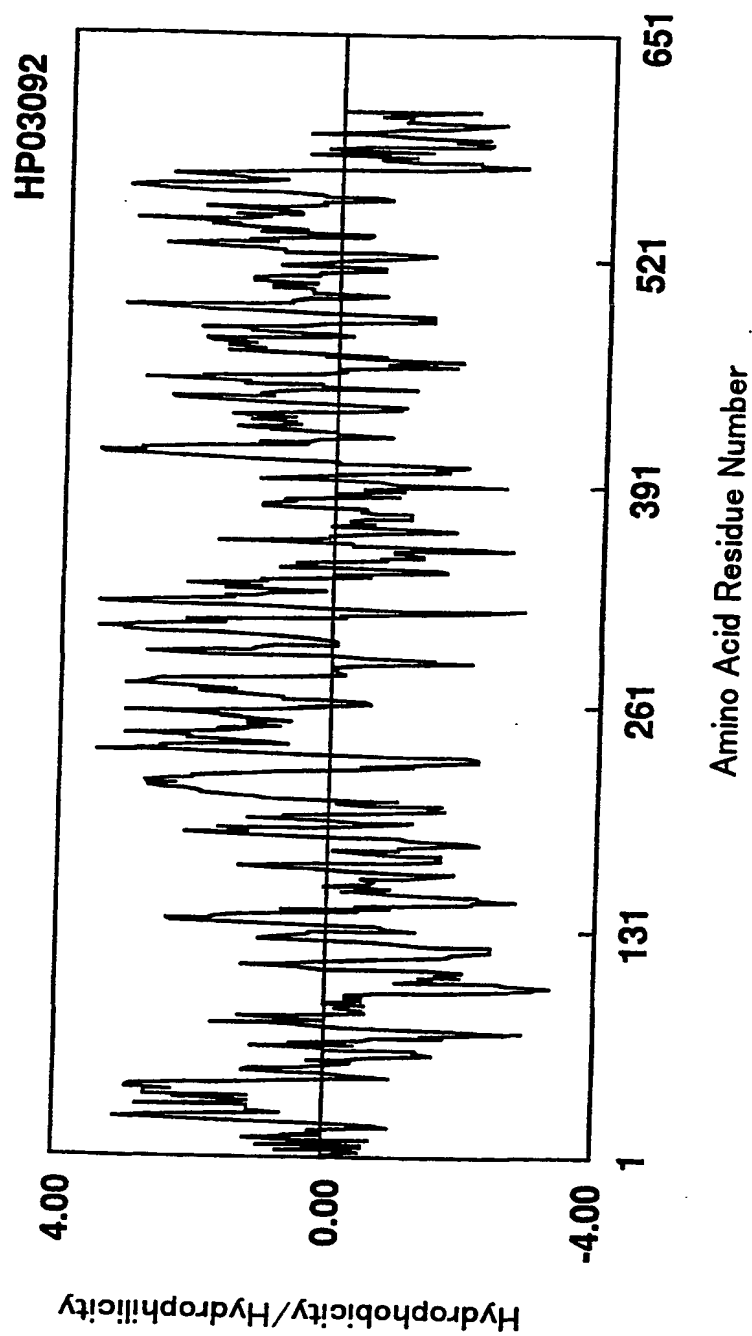
14/50

Fig.14



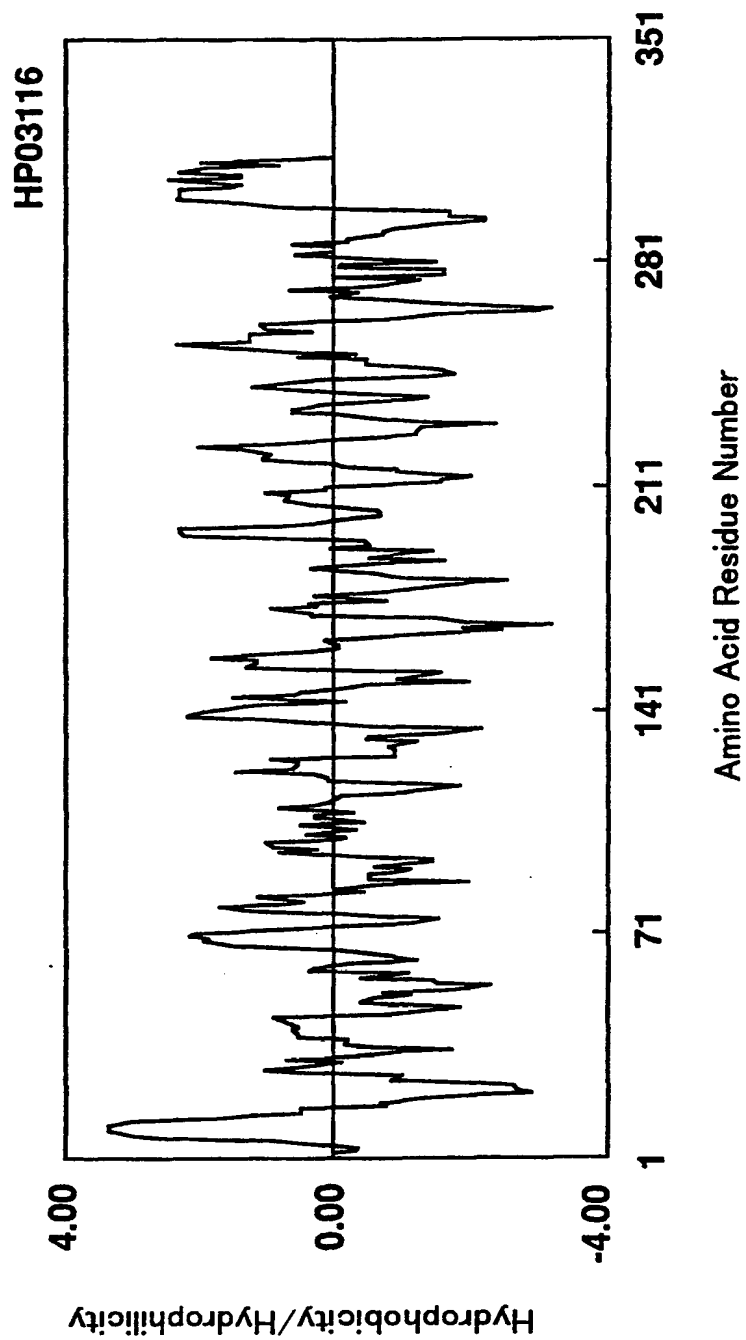
15/50

Fig.15



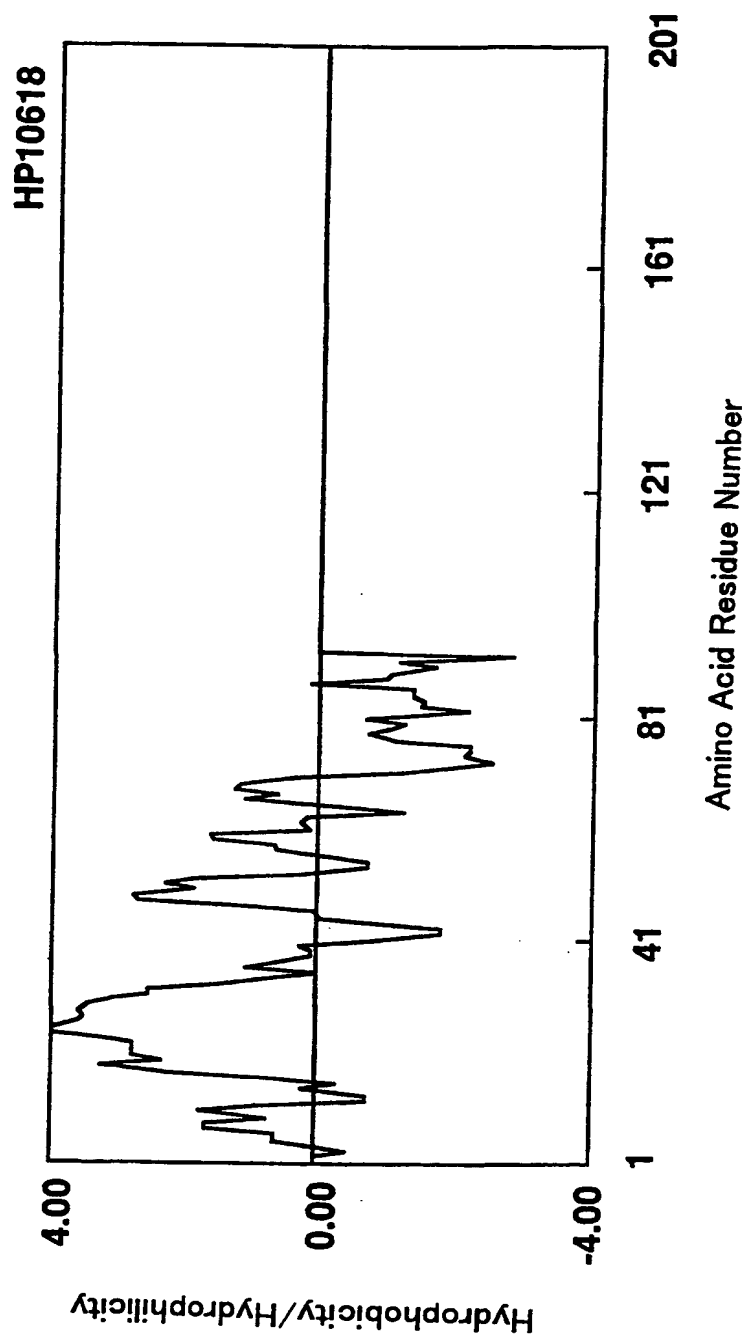
16/50

Fig.16

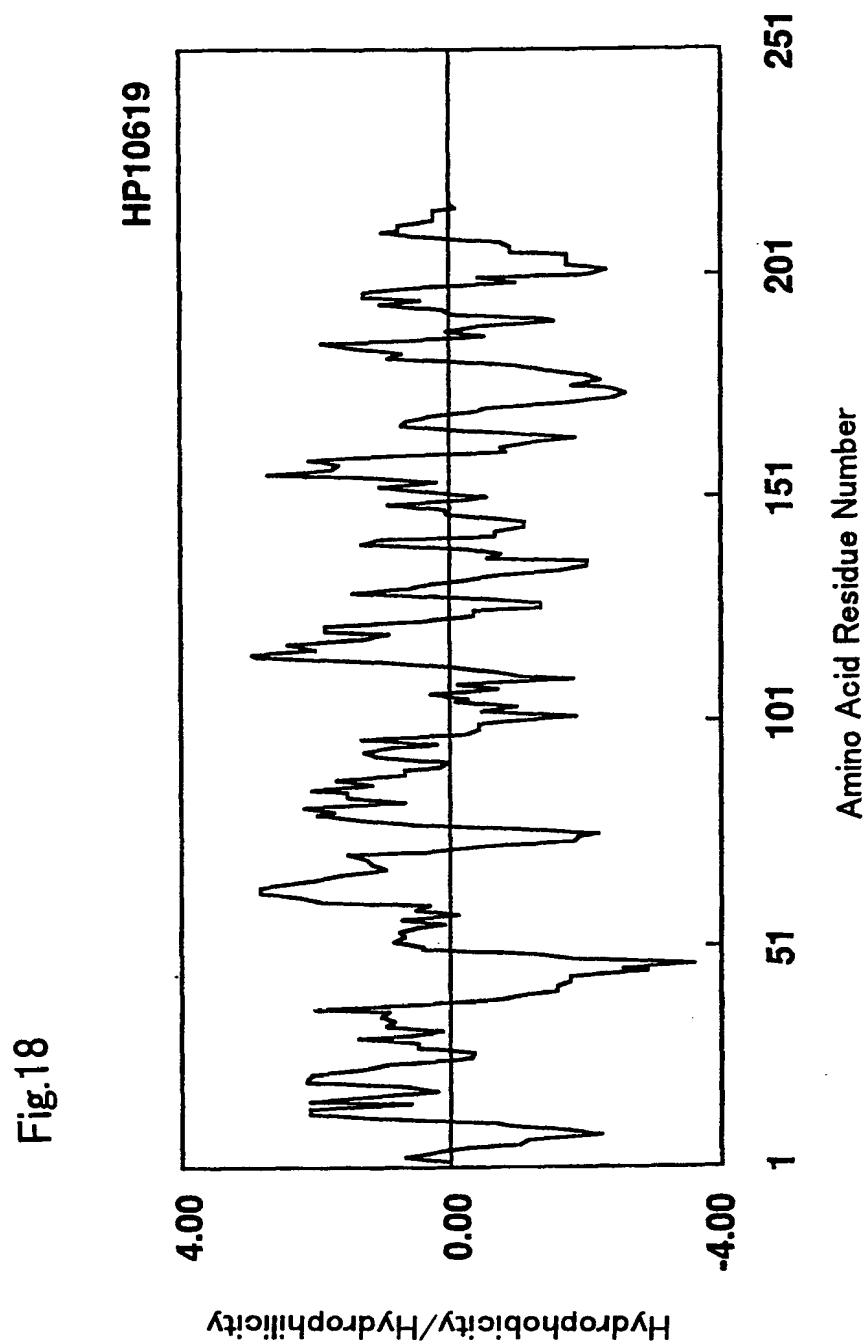


17/50

Fig.17

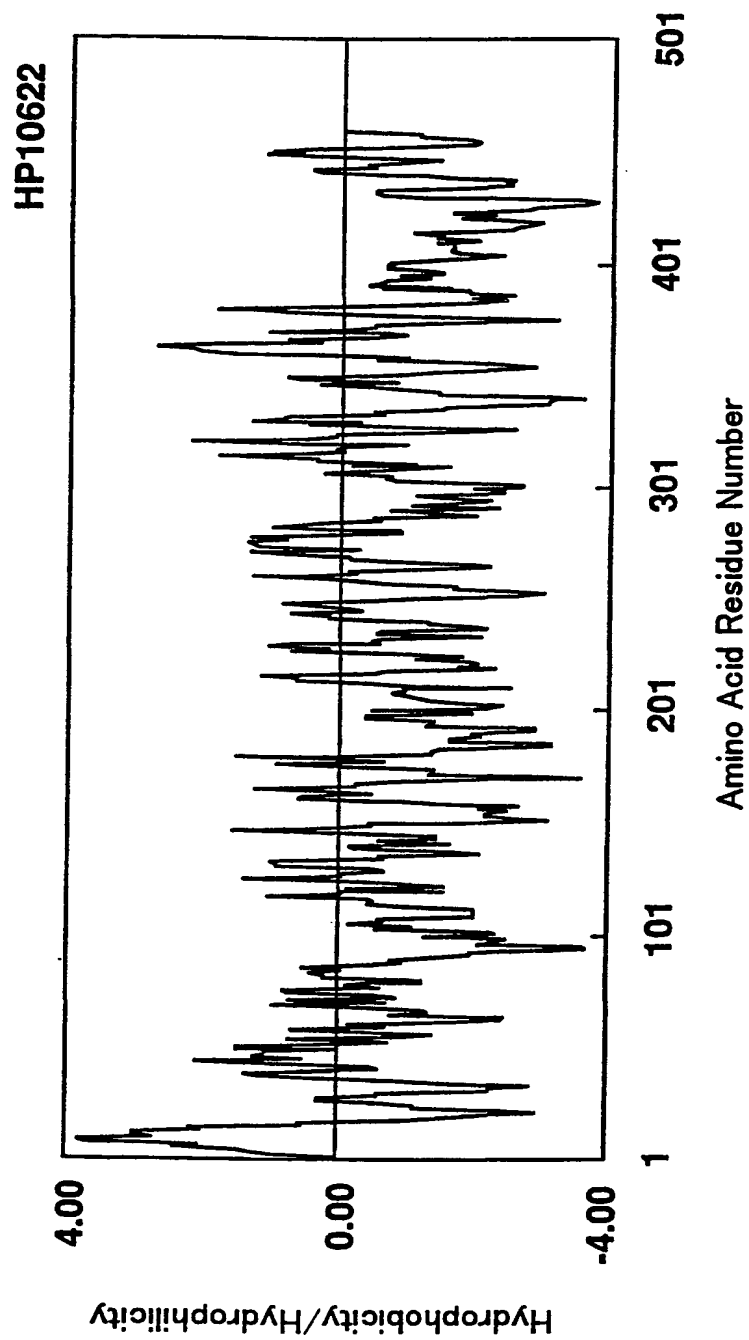


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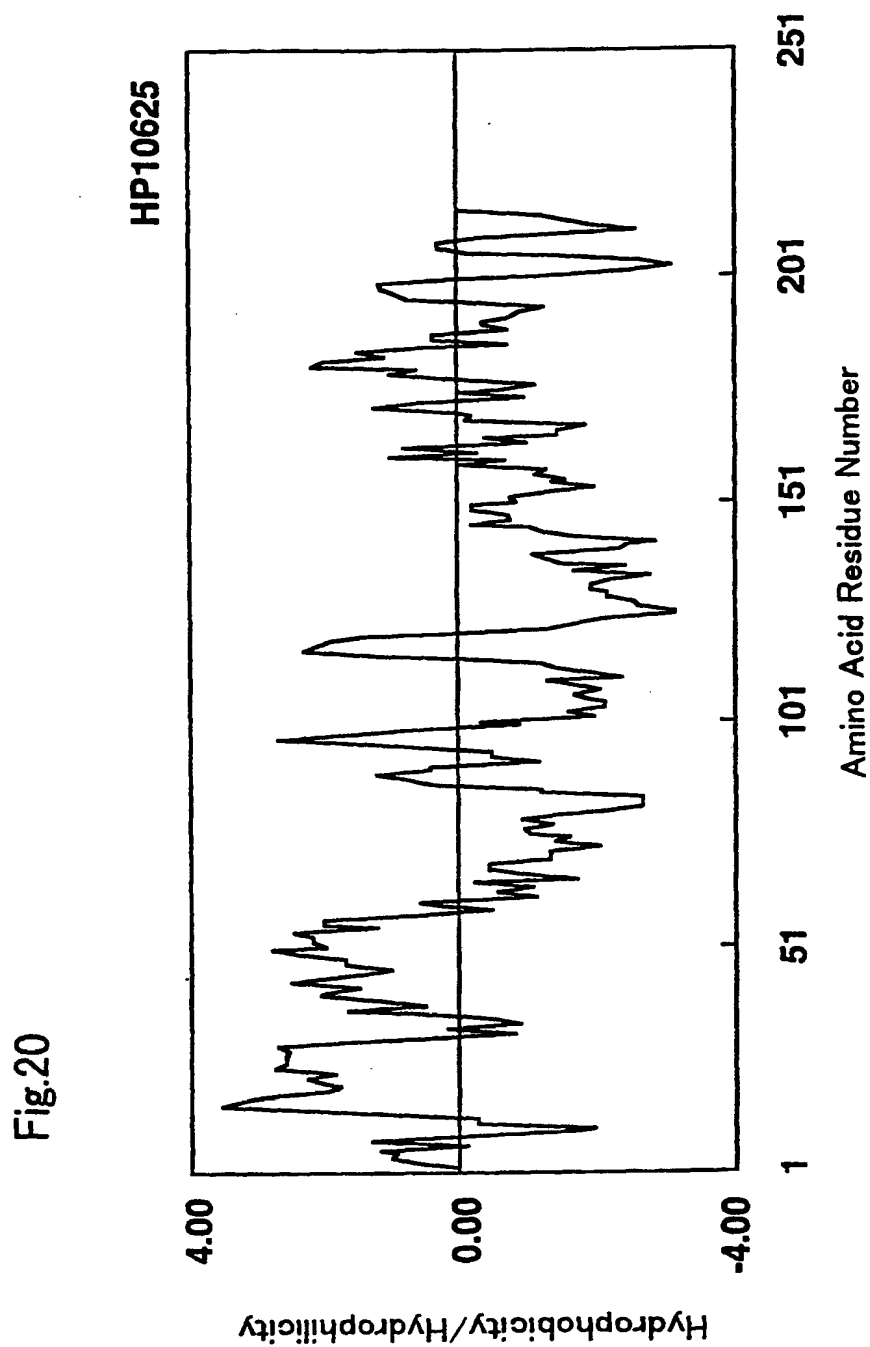


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Fig.19

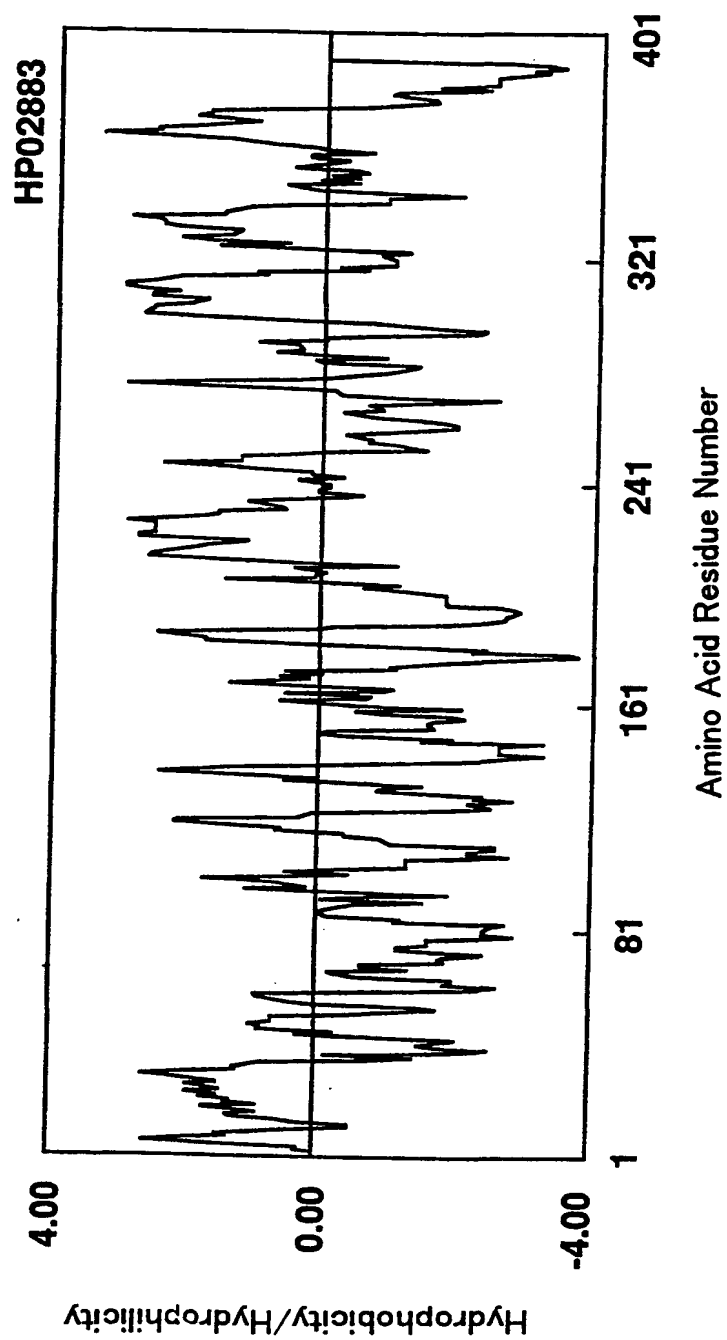


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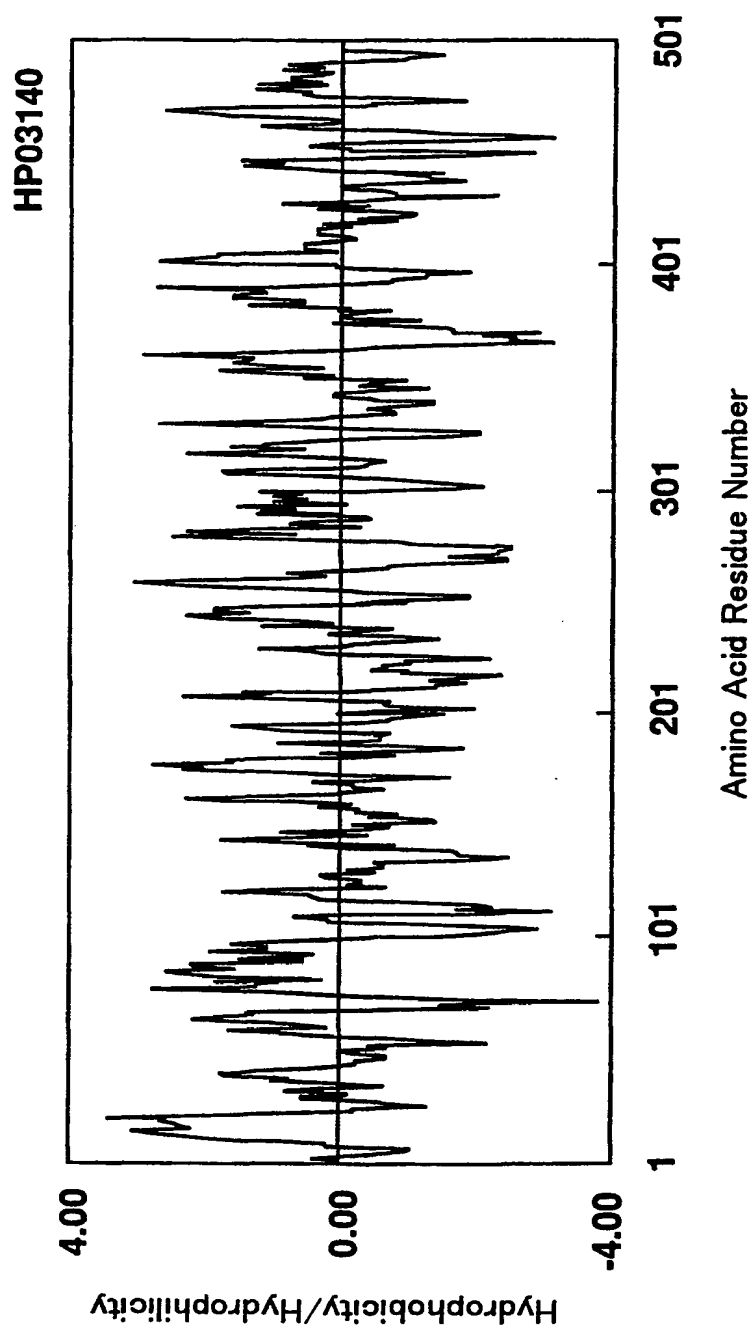
21/50

Fig.21



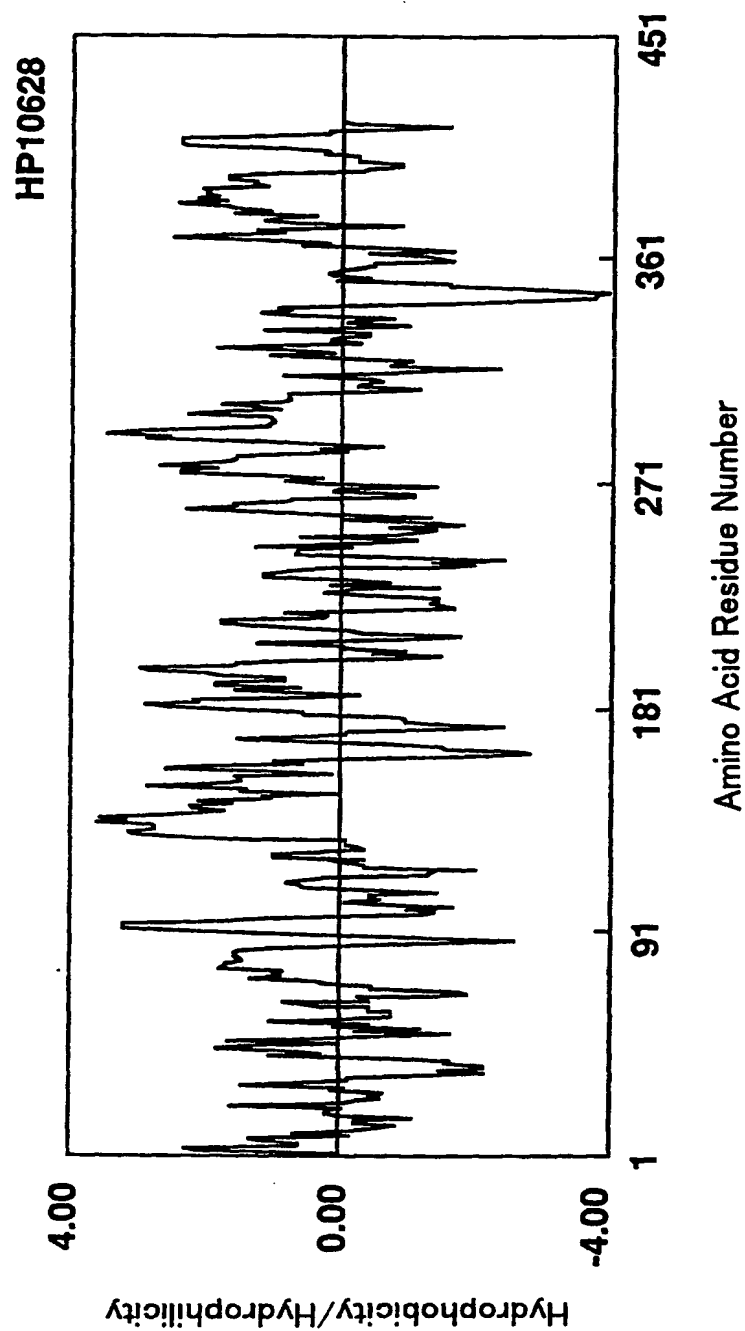
22/50

Fig.22



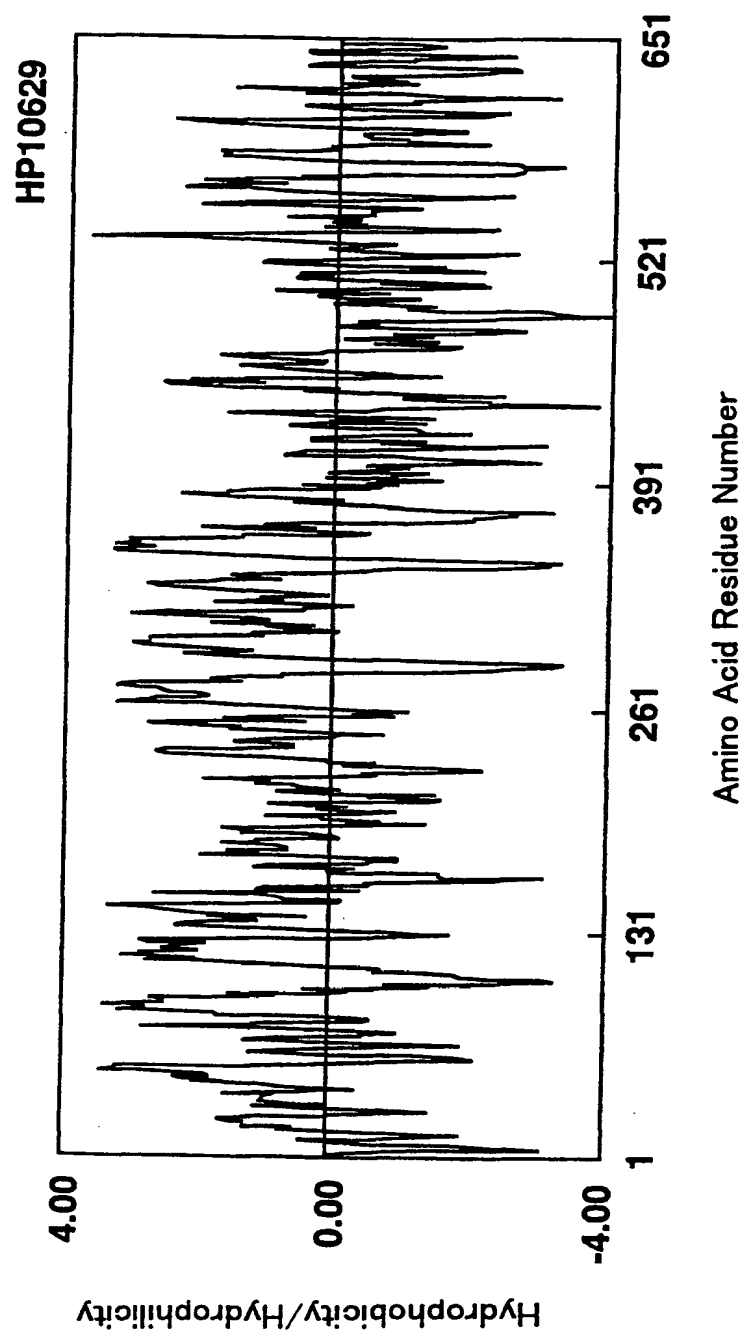
23/50

Fig.23



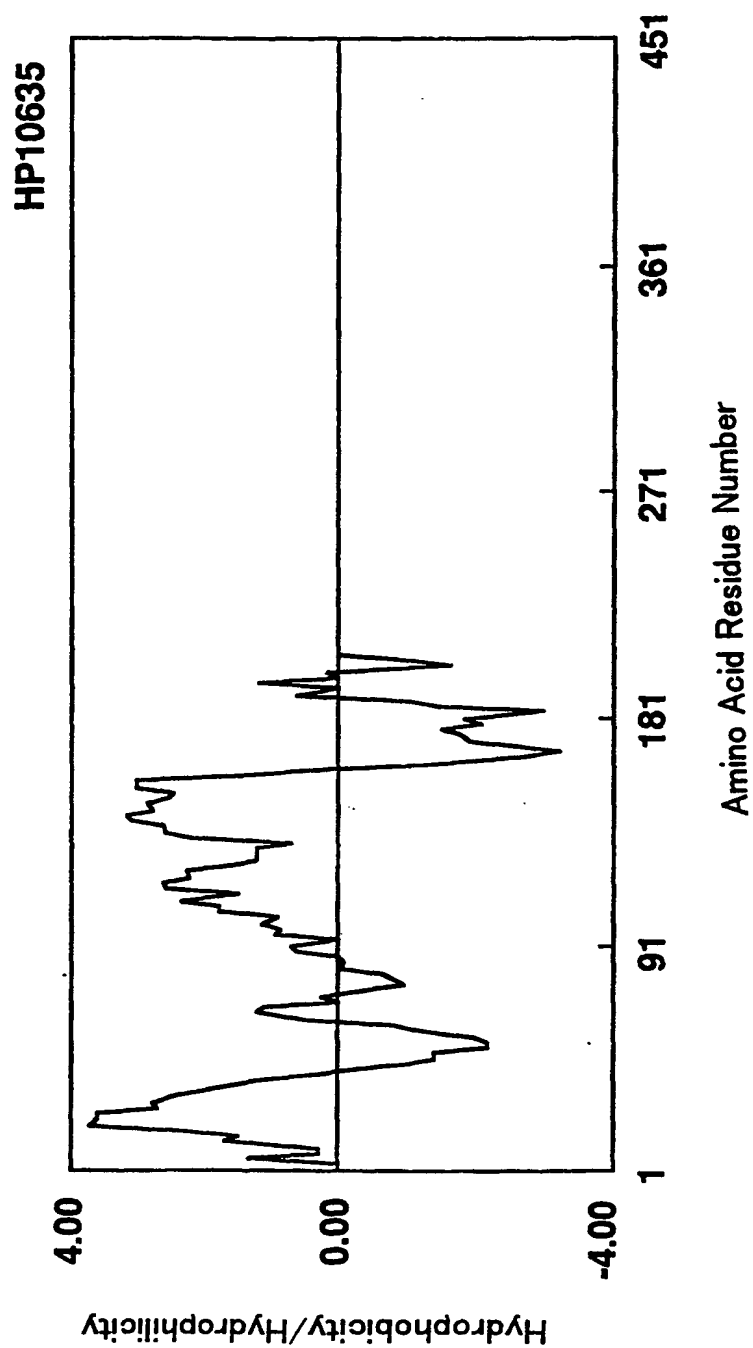
24/50

Fig.24



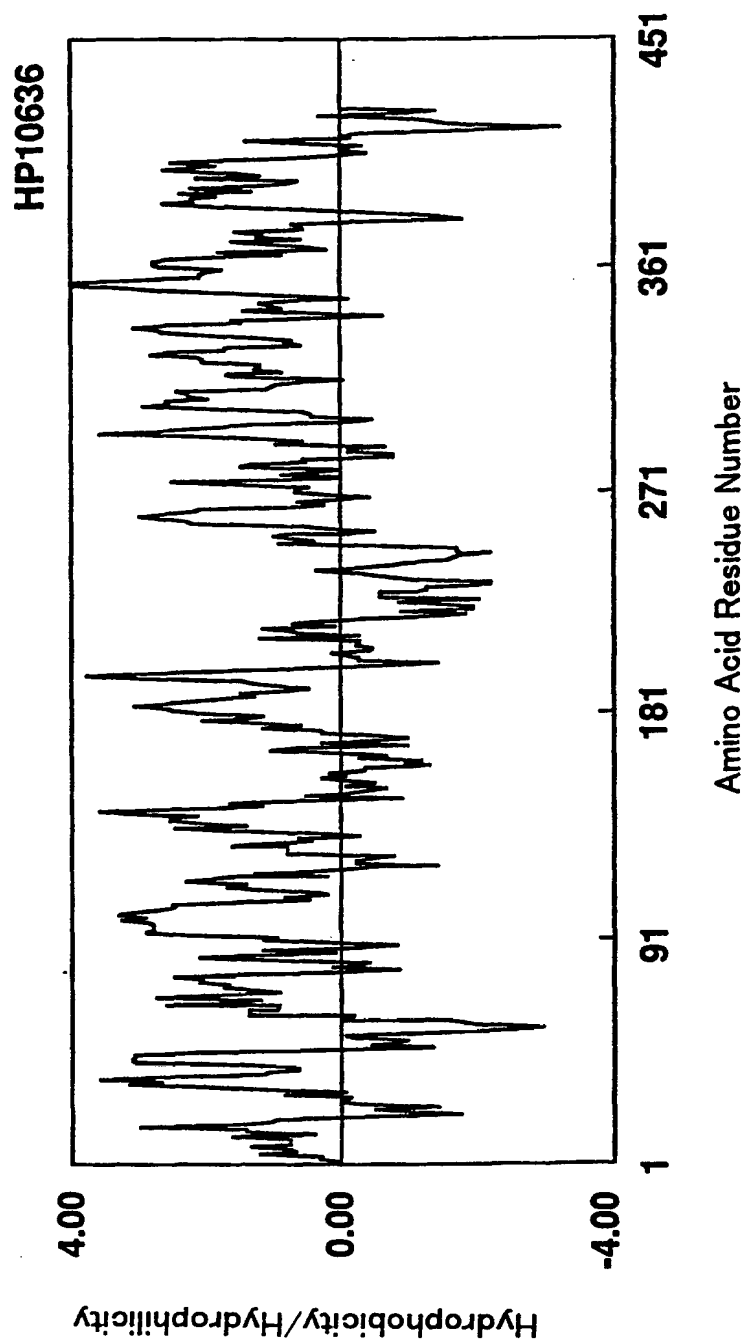
25/50

Fig.25



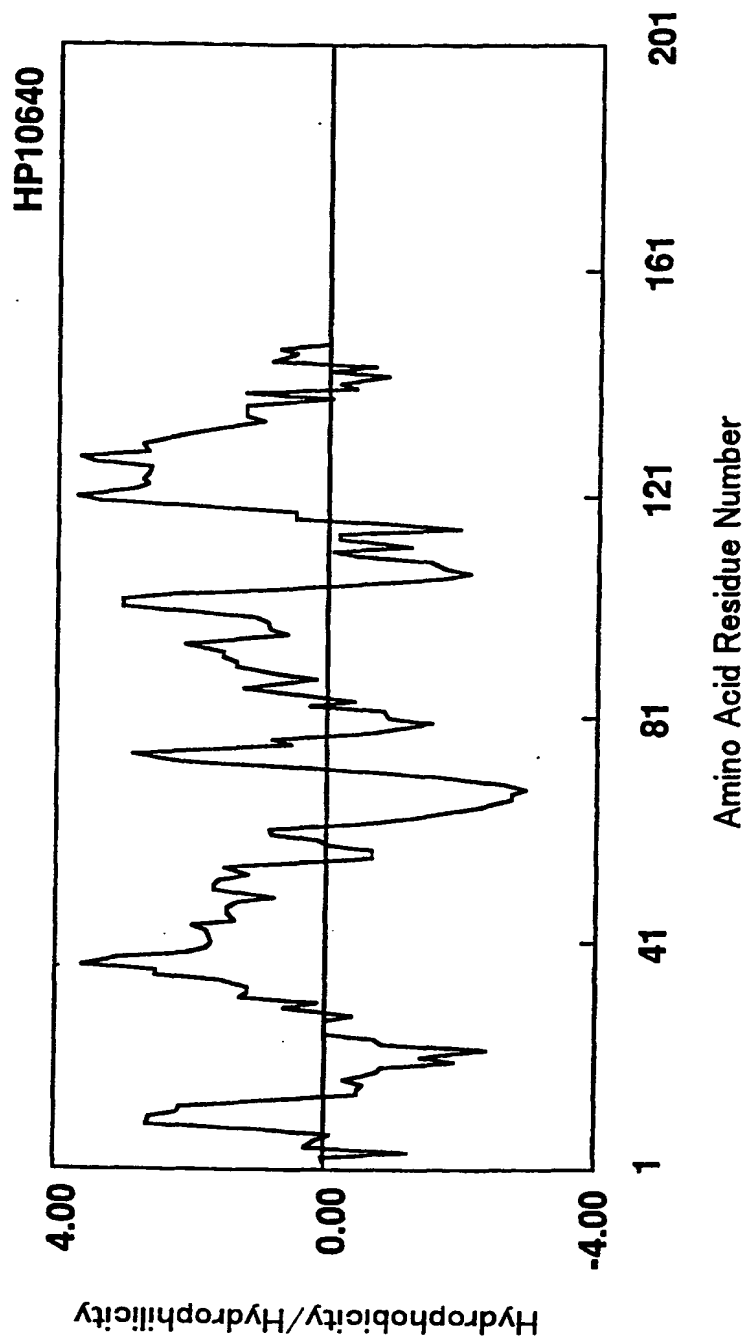
26/50

Fig.26



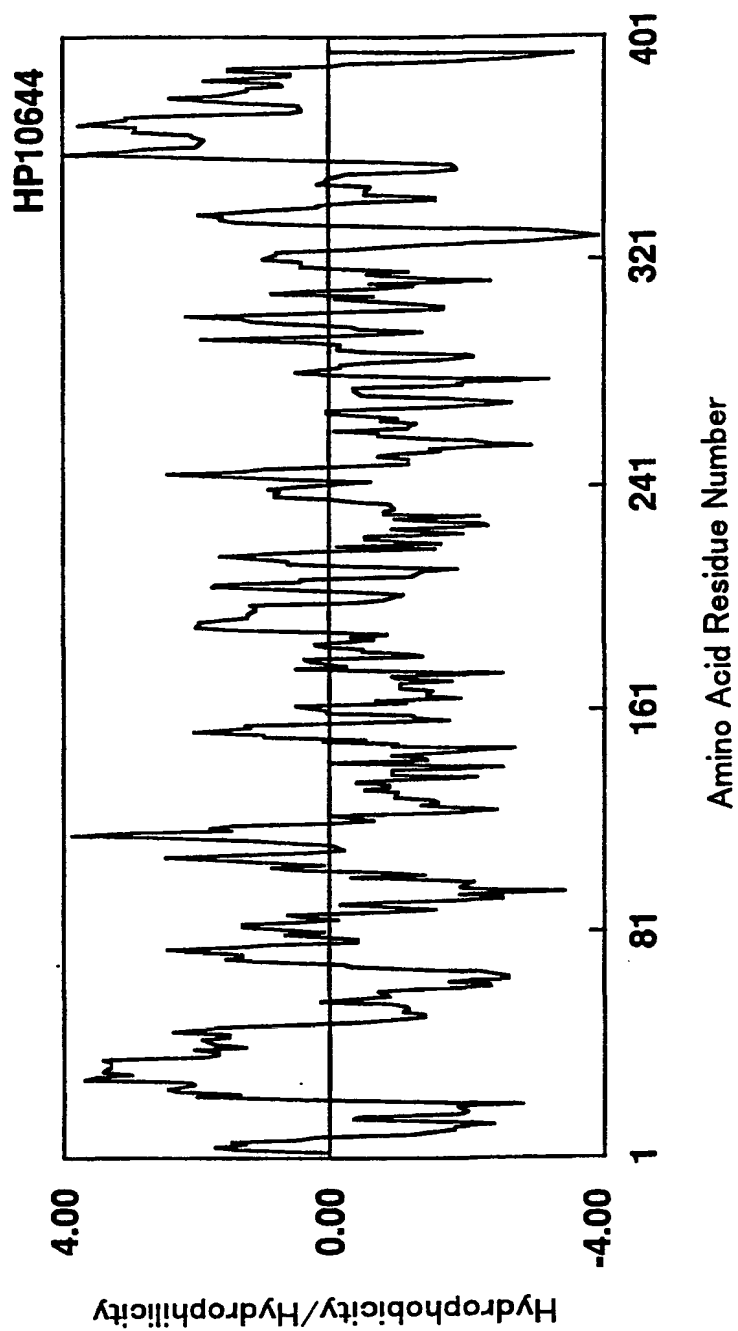
27/50

Fig.27



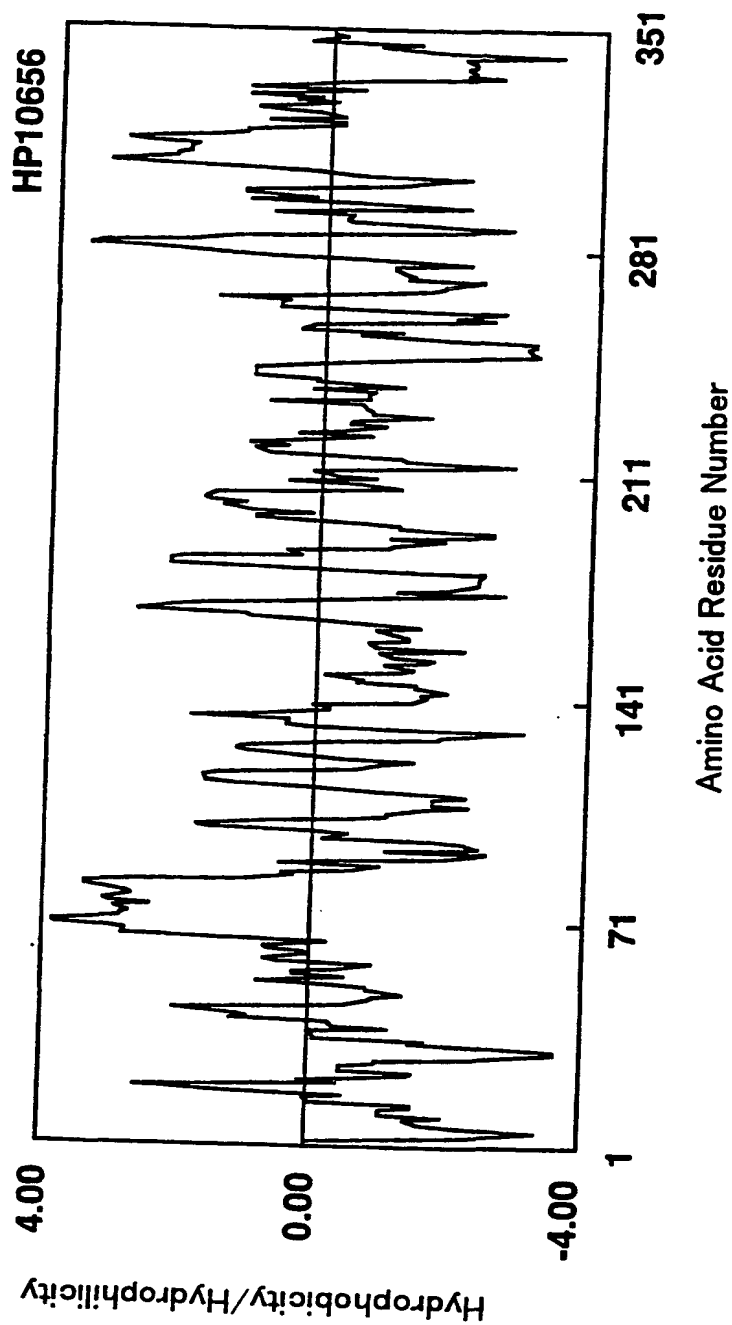
28/50

Fig.28



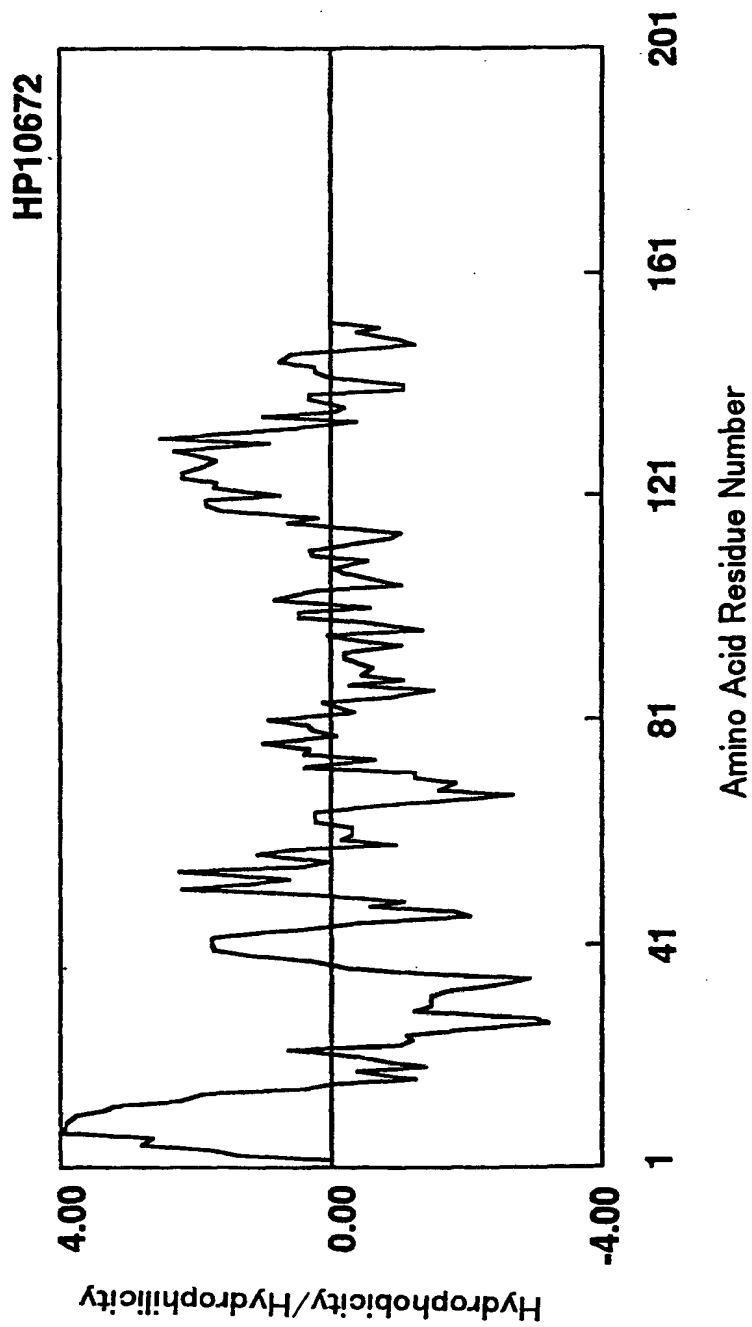
29/50

Fig.29

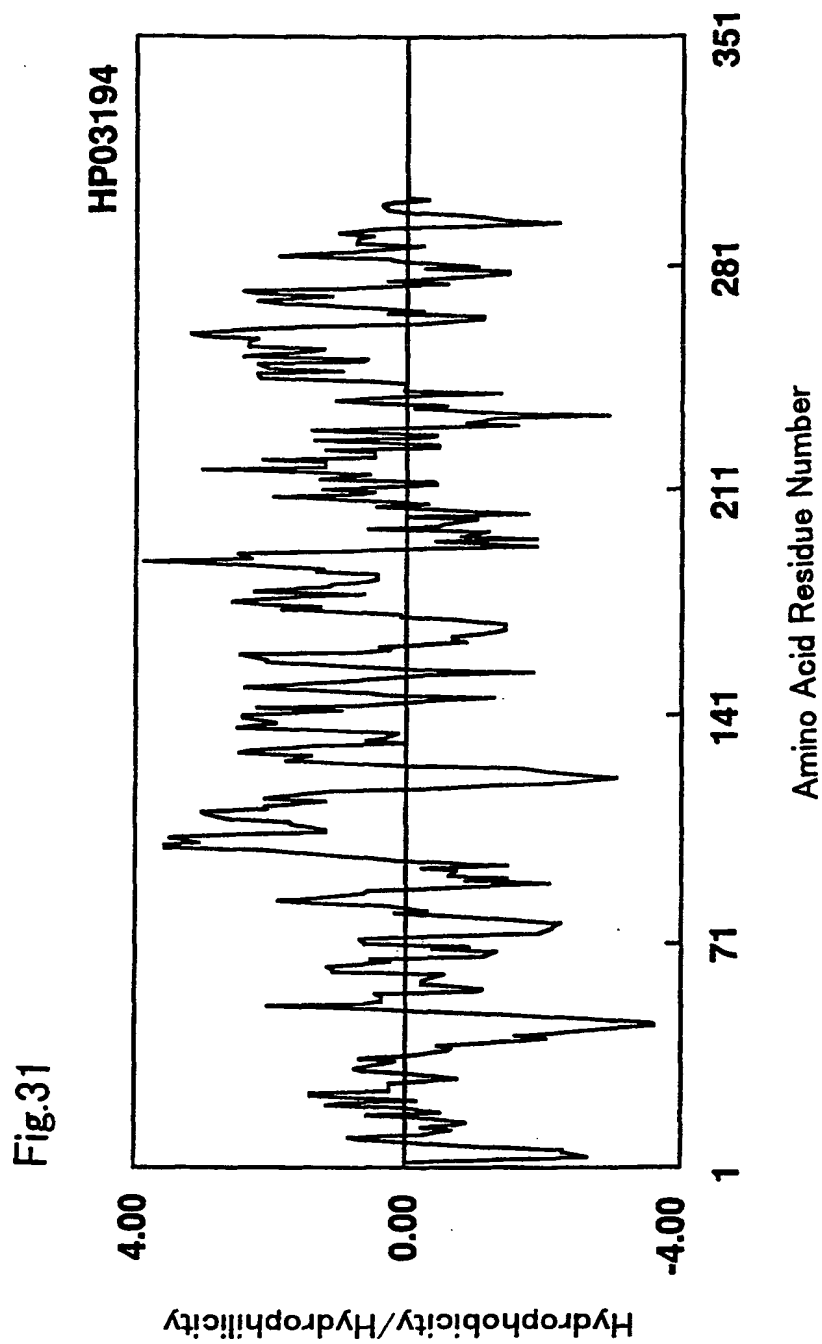


30/50

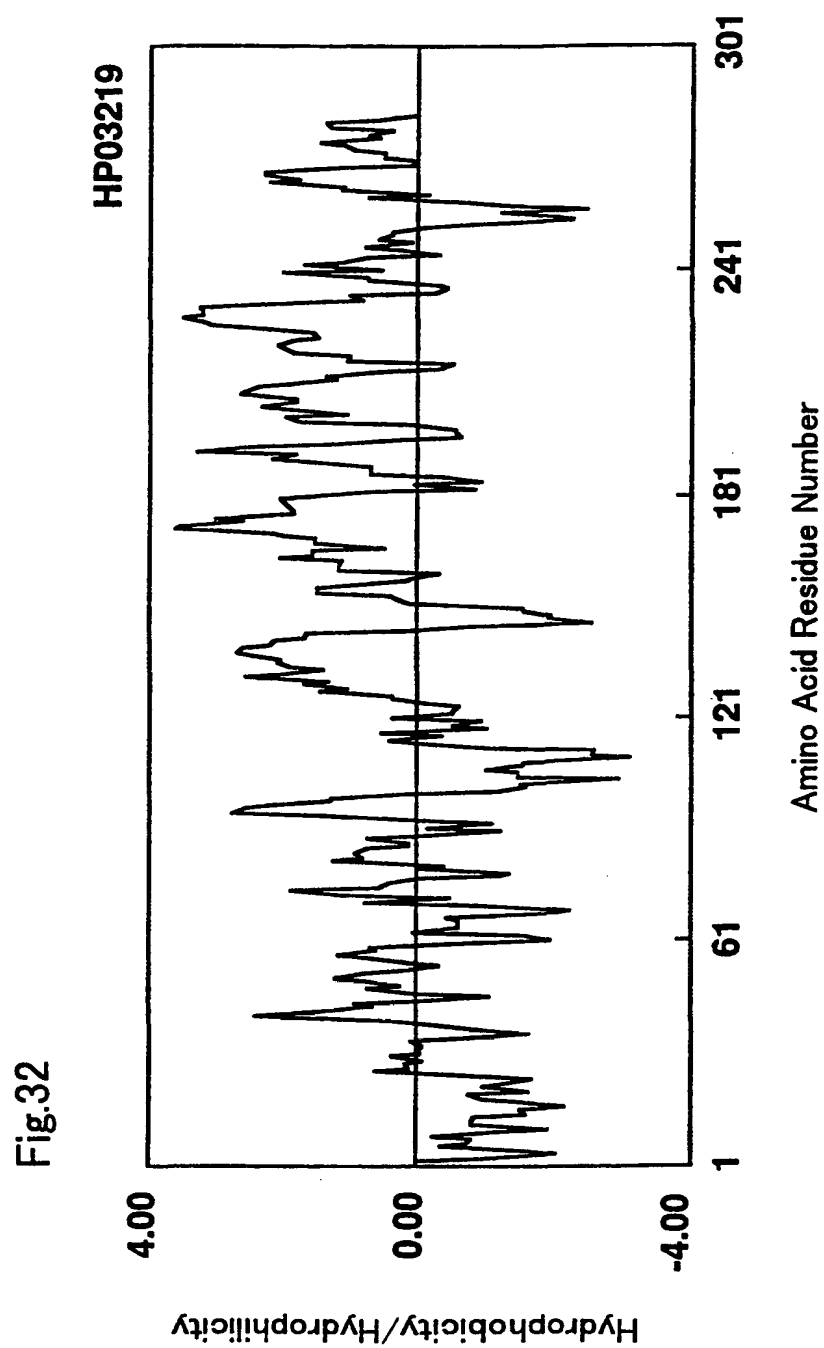
Fig.30



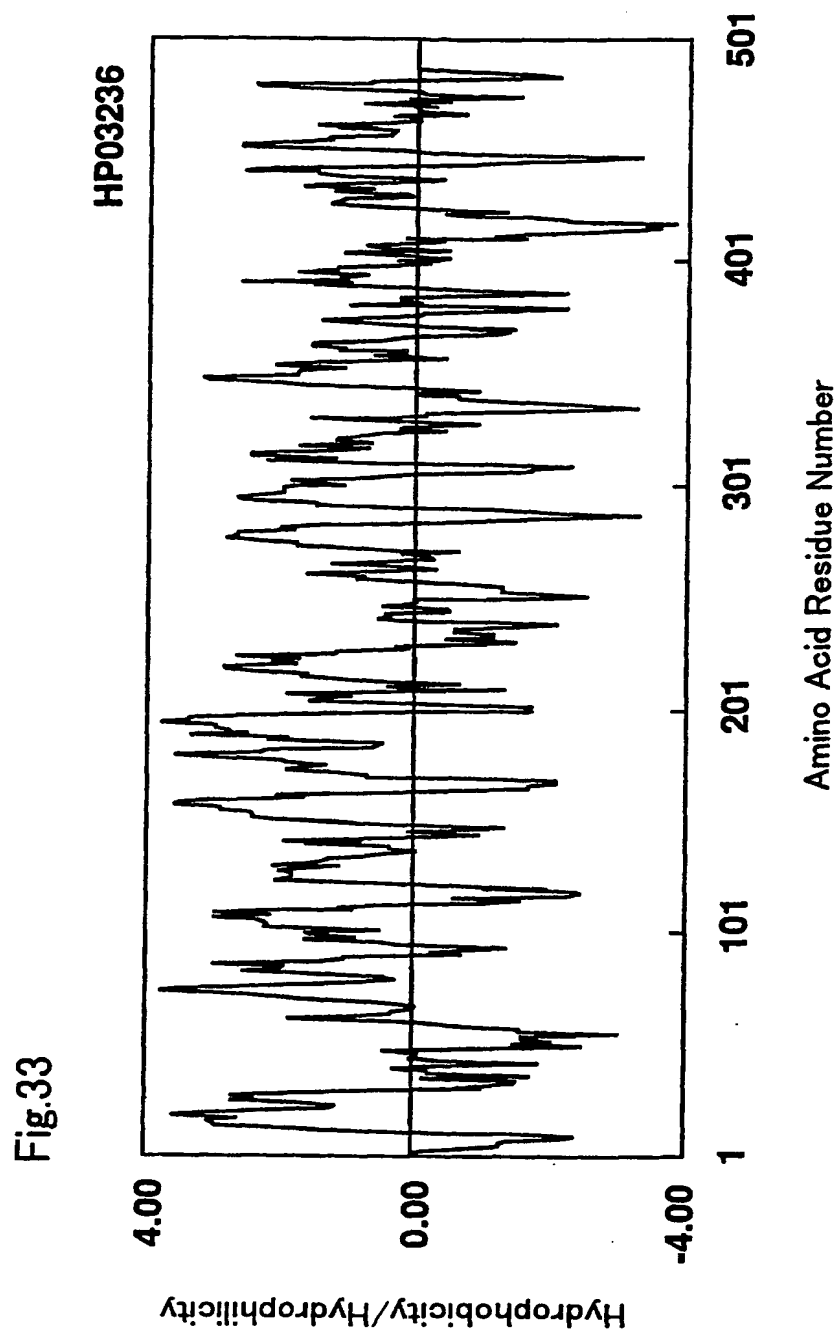
31/50



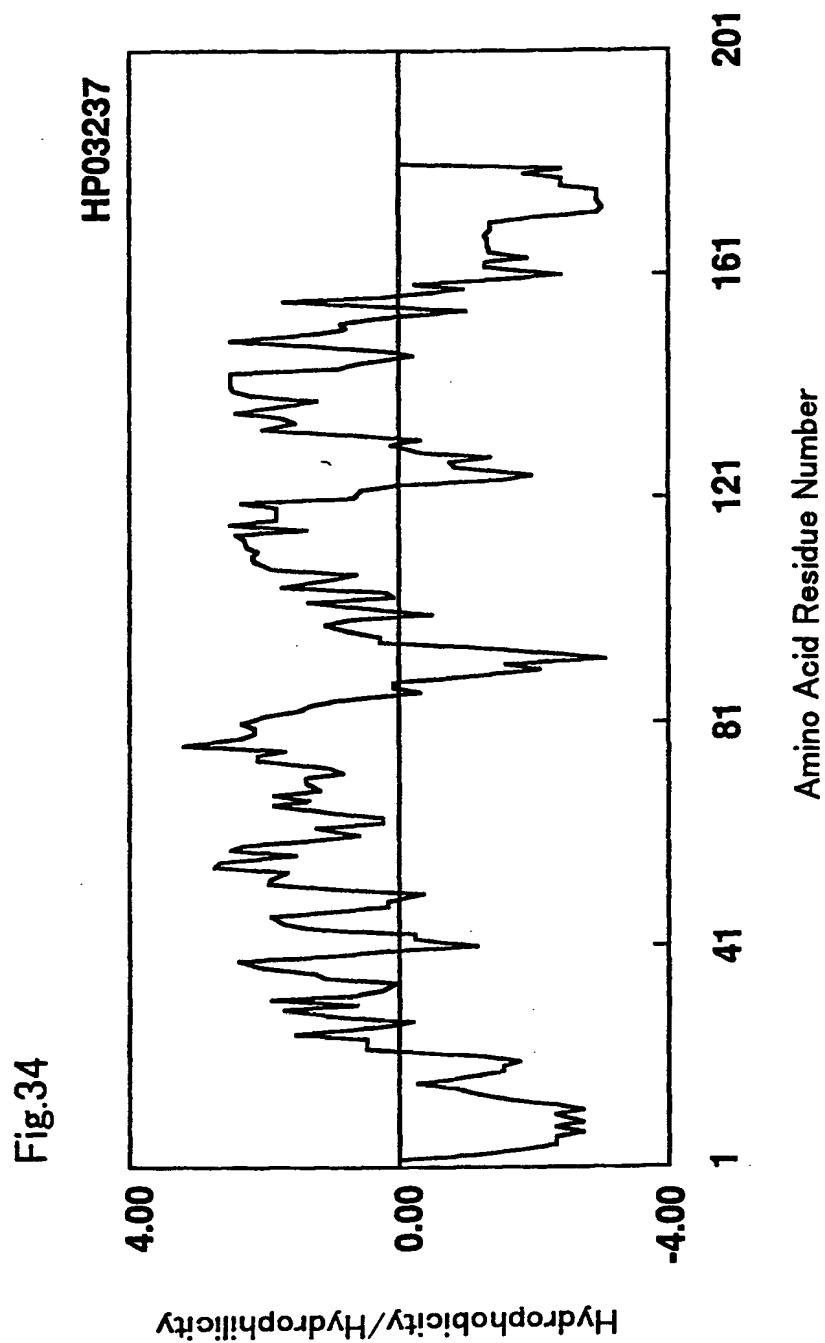
32/50



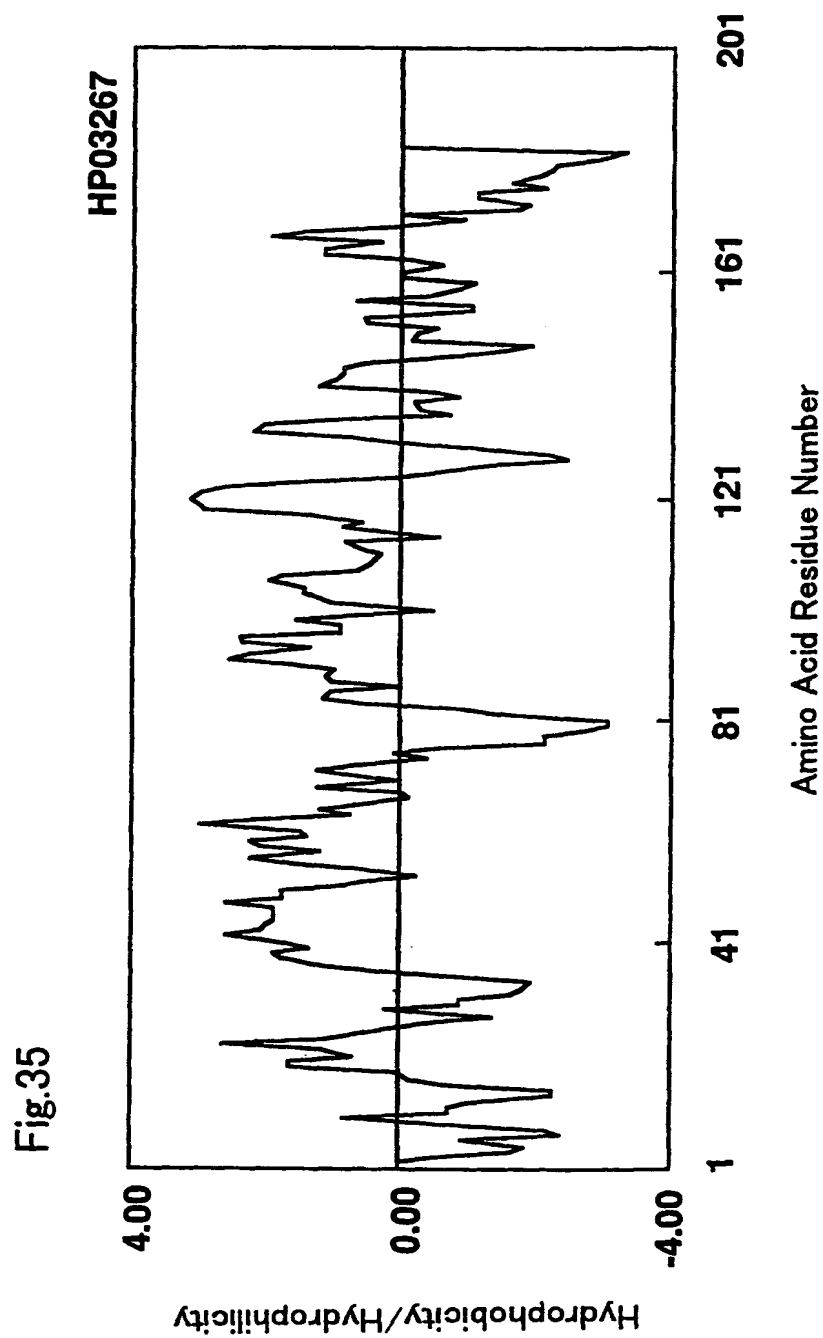
33/50



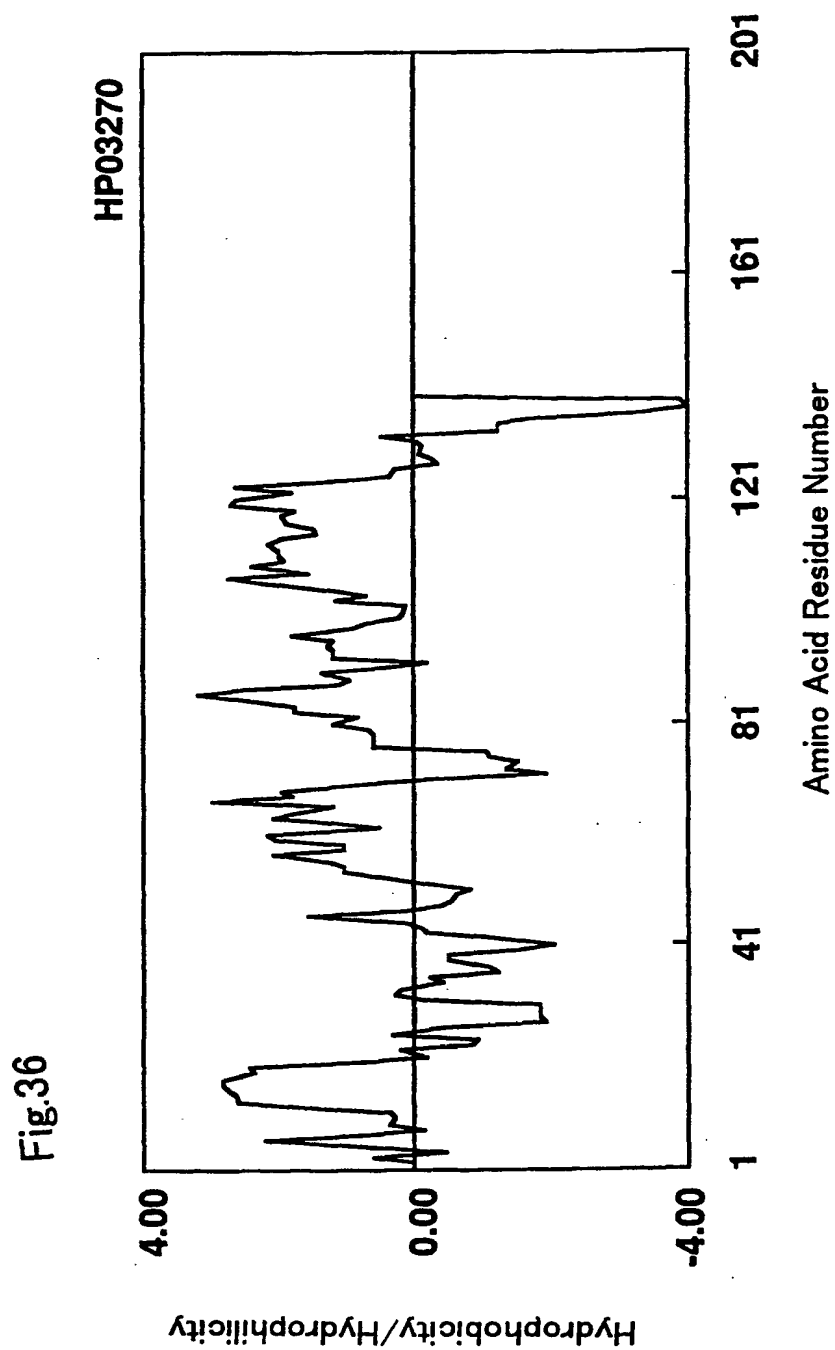
34/50



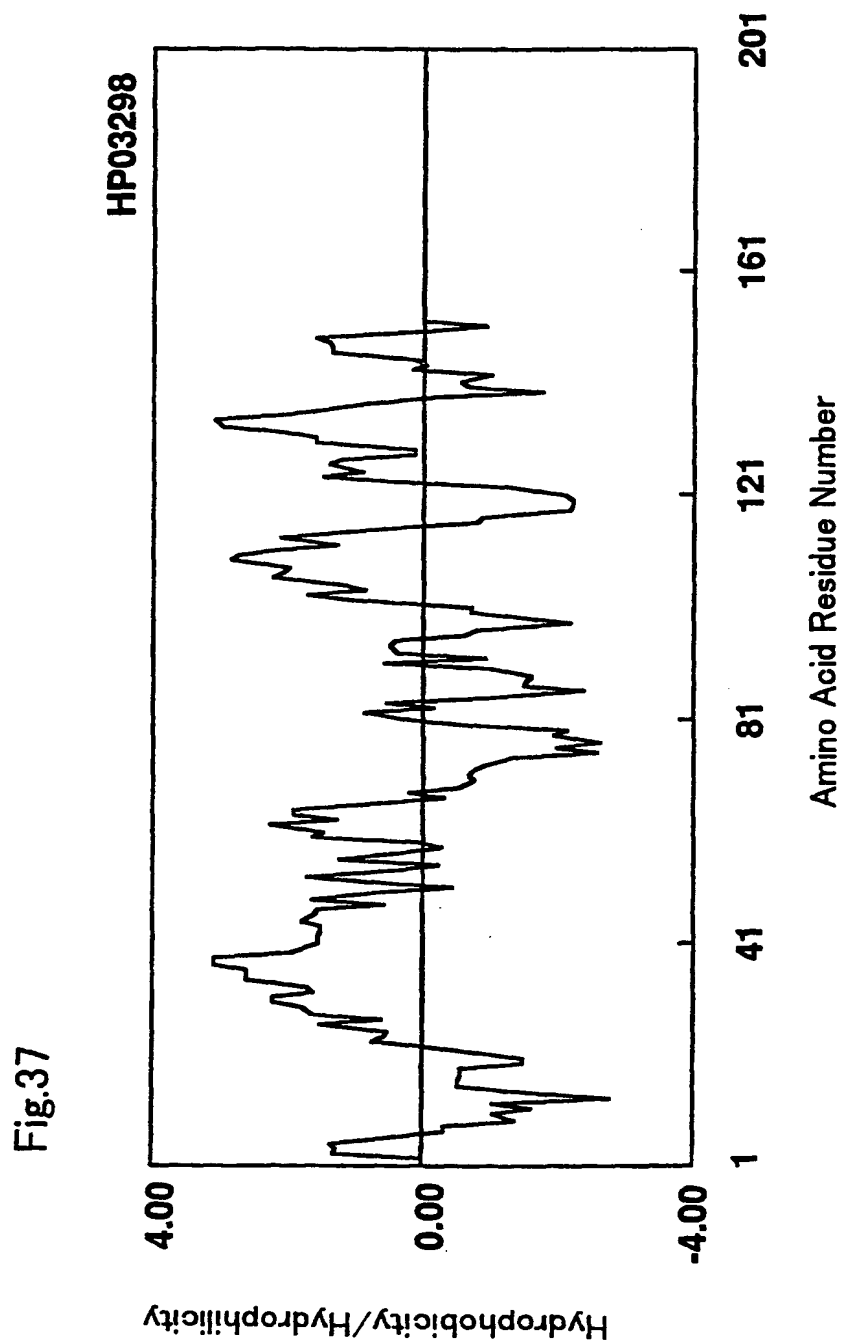
35/50



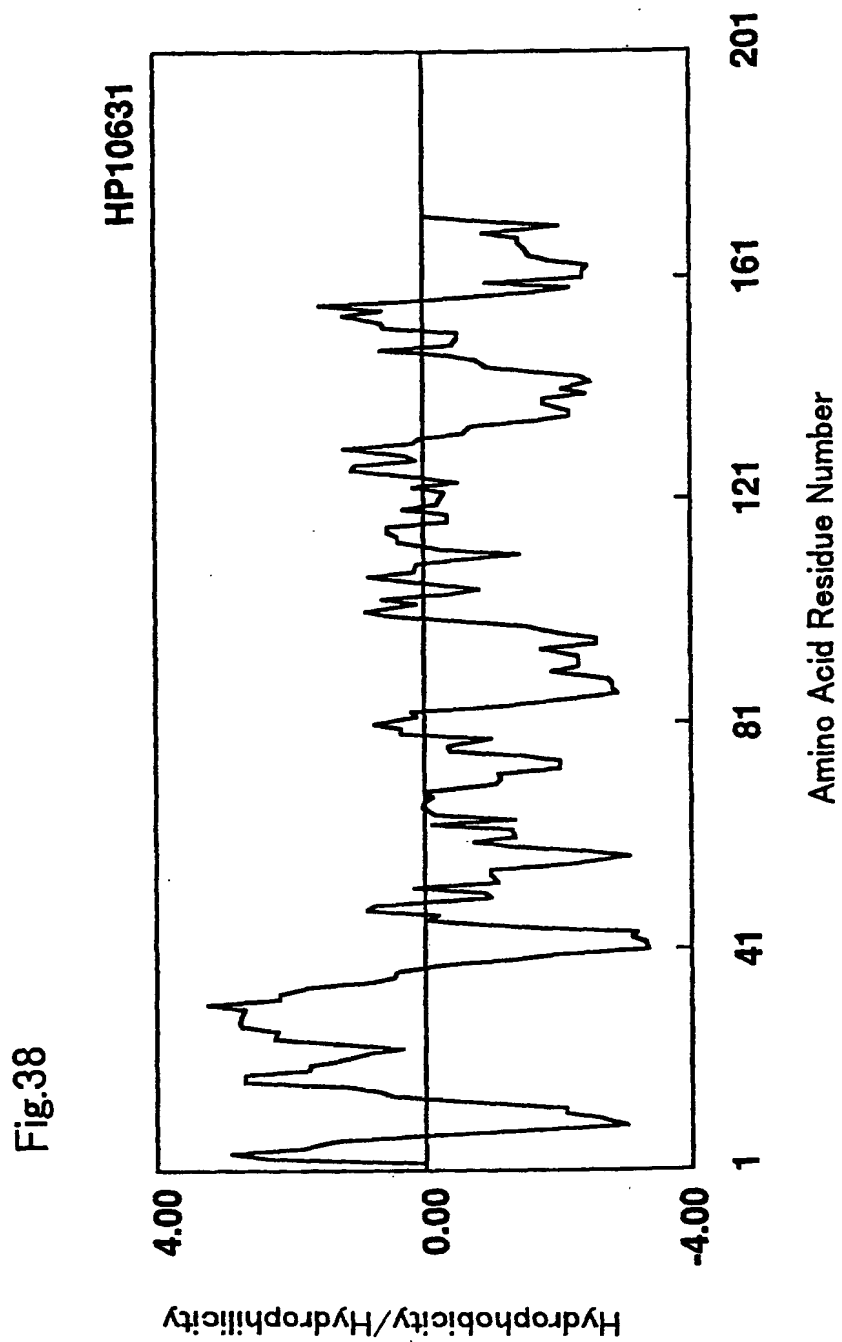
36/50



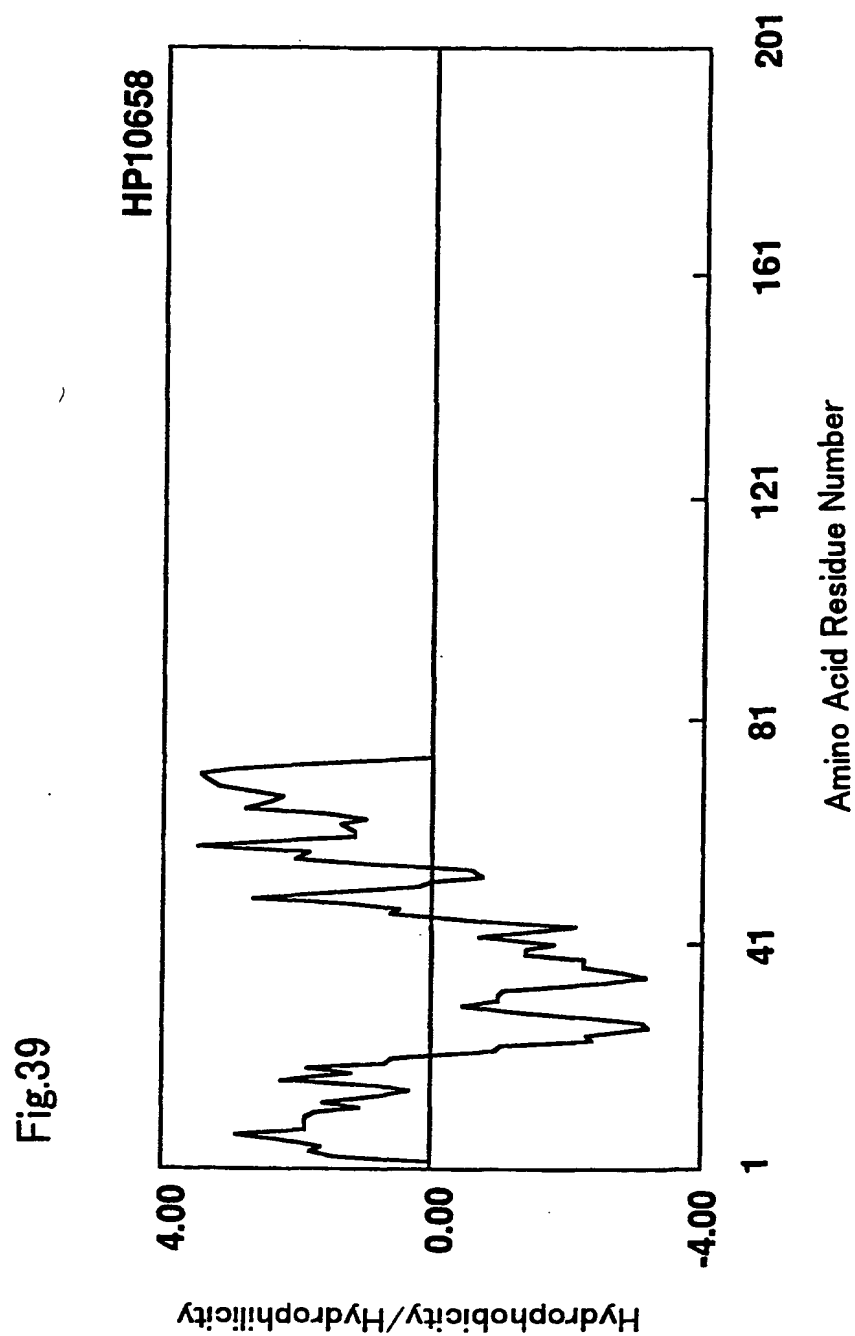
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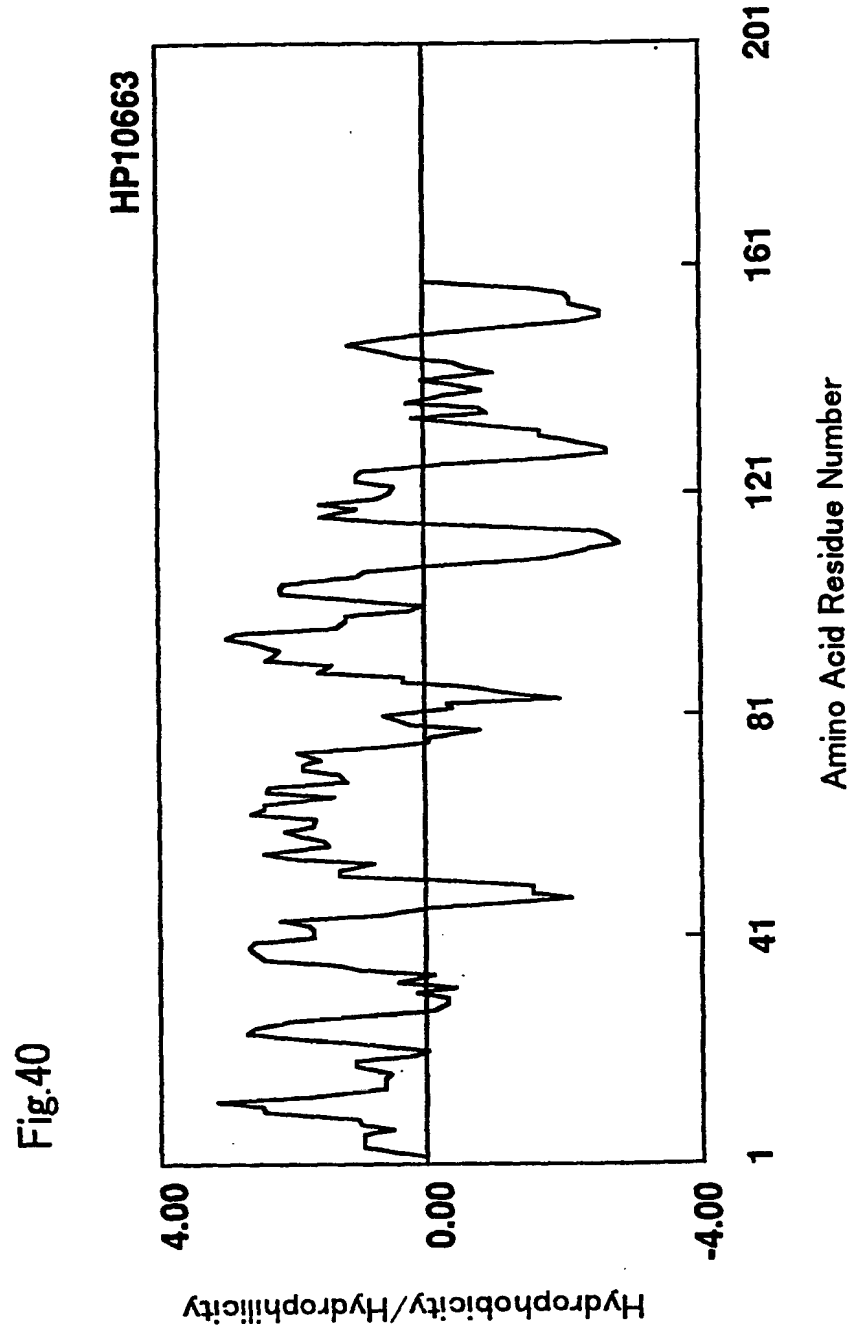
38/50



39/50

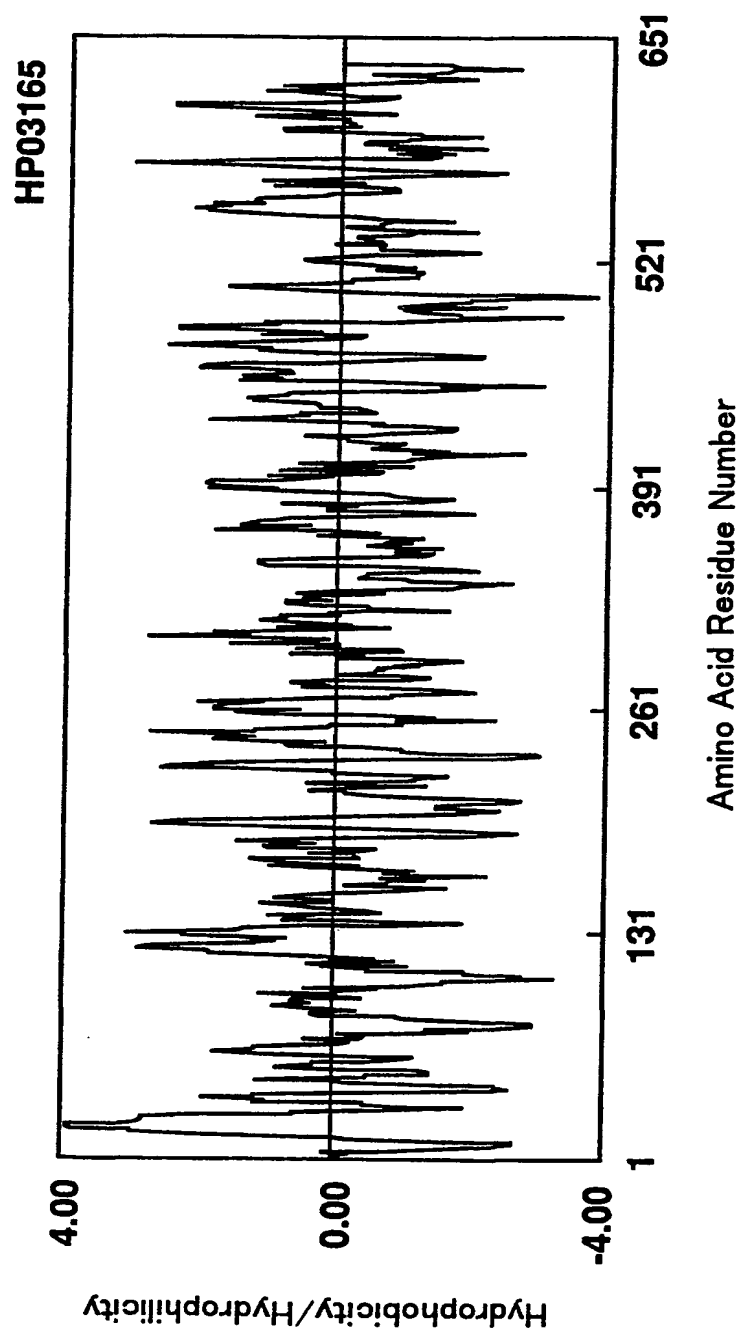


40/50

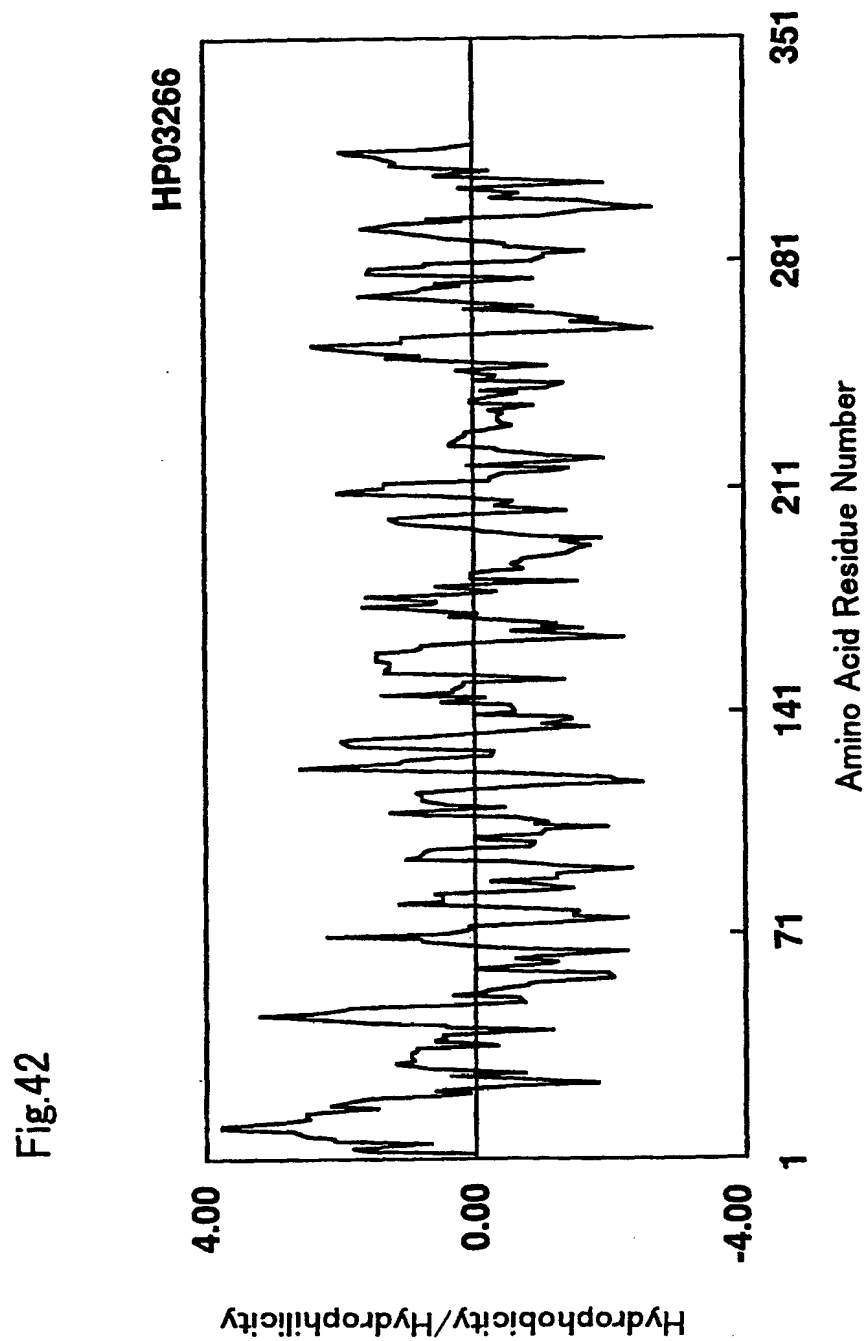


41/50

Fig.41

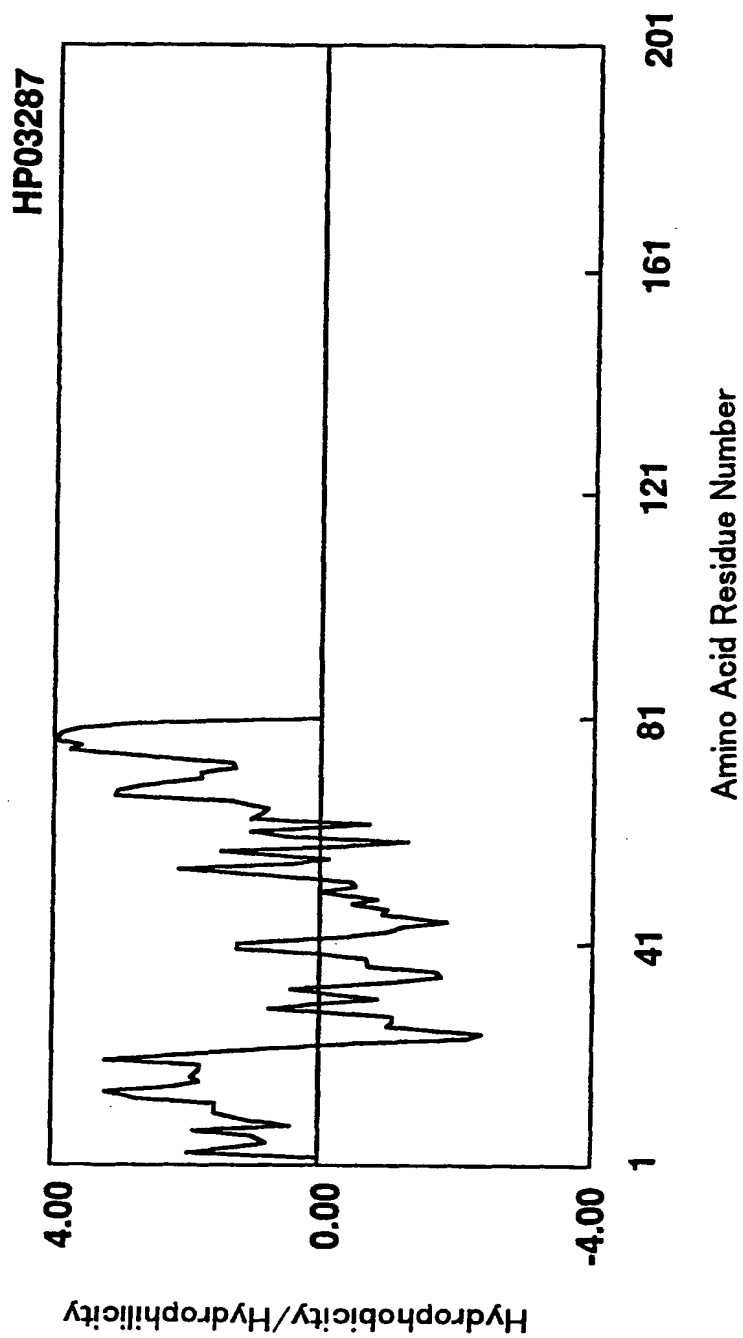


42/50

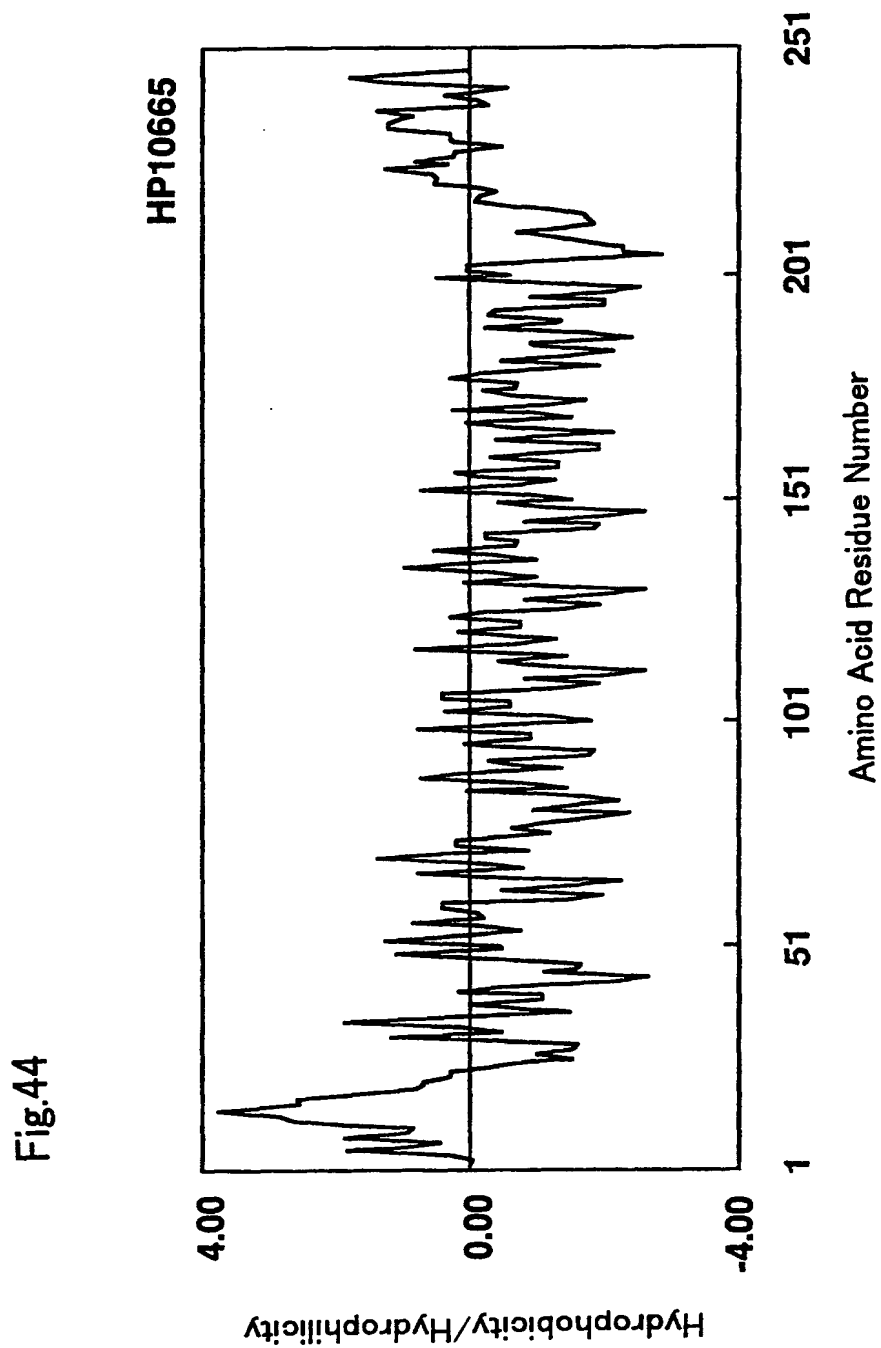


43/50

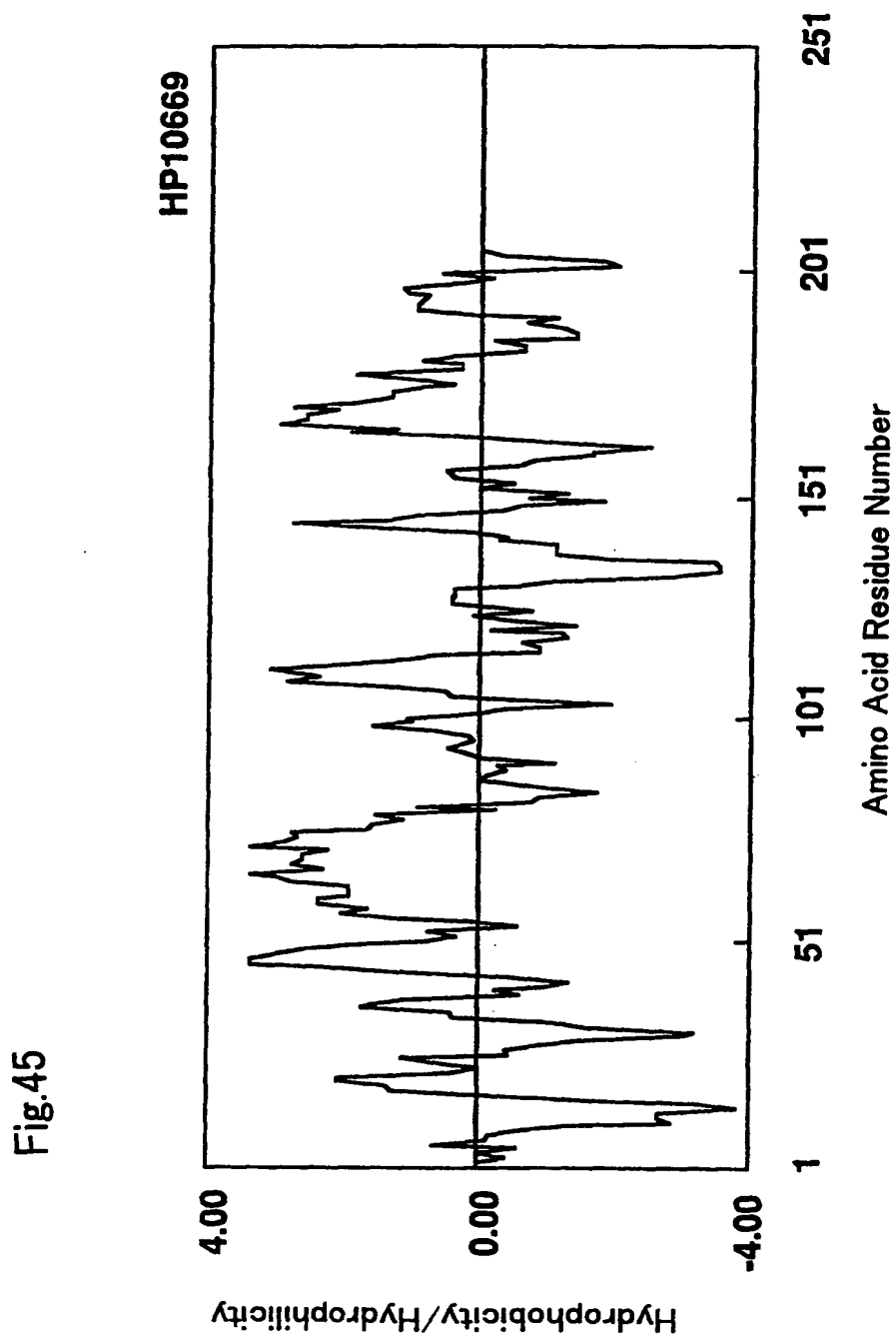
Fig.43



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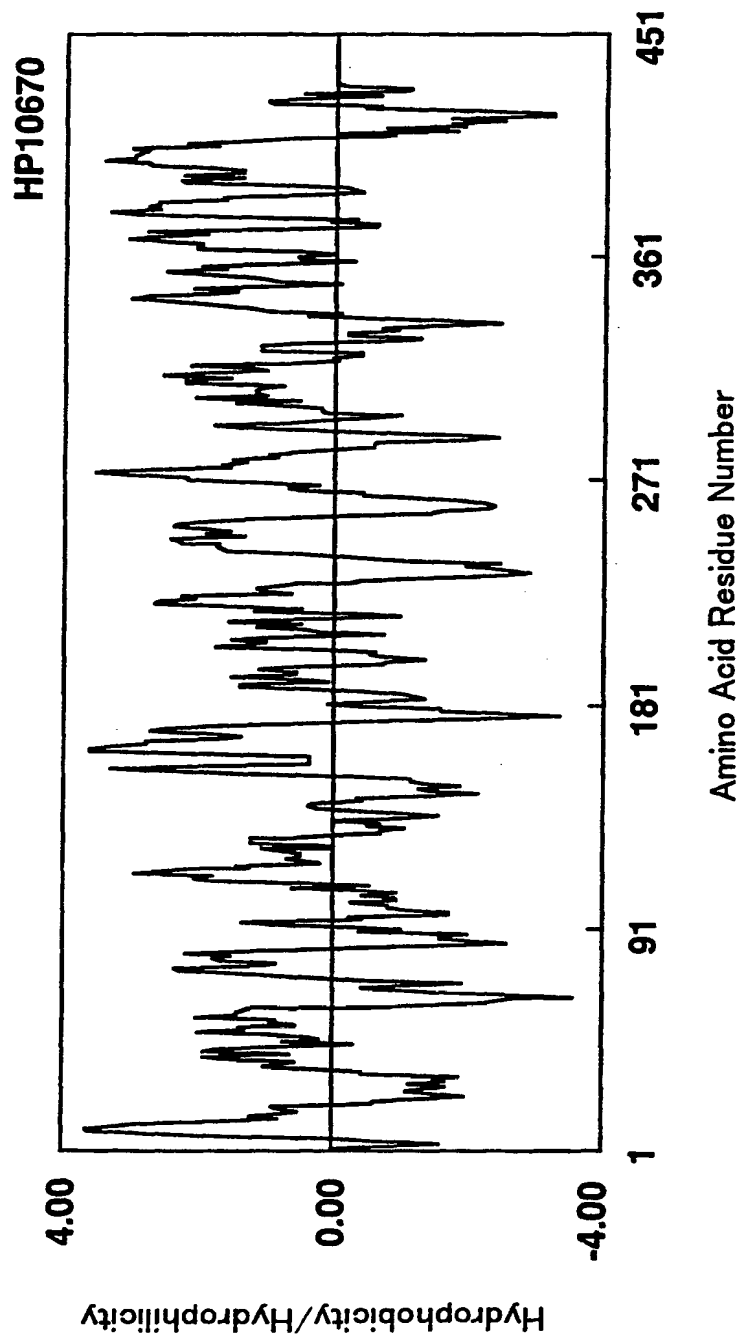


45/50



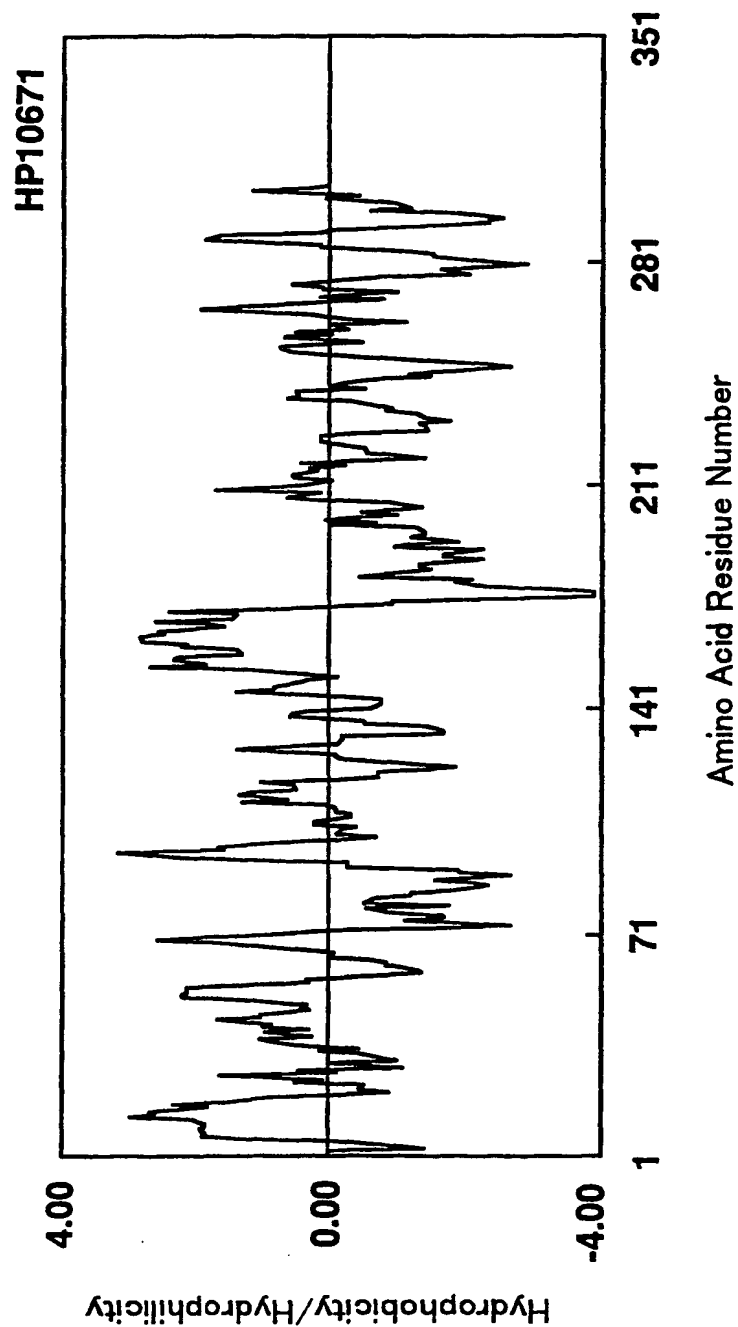
46/50

Fig.46



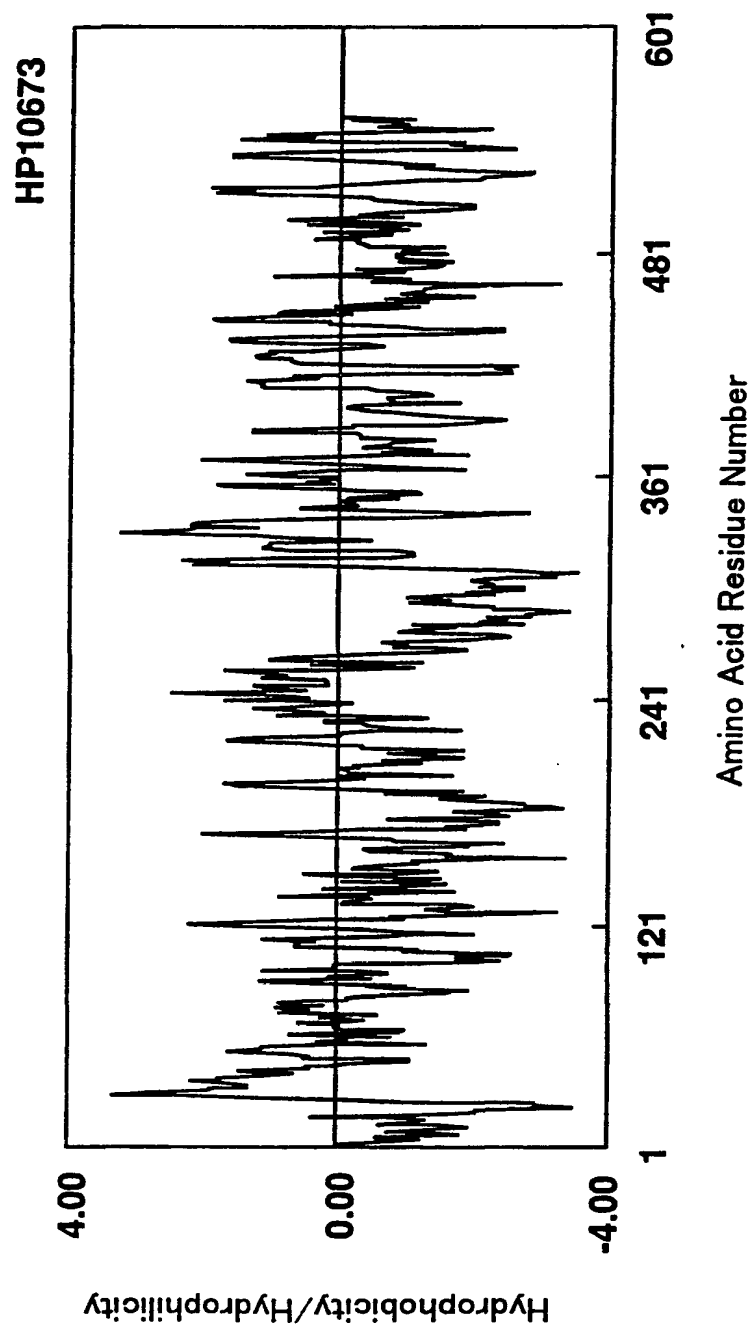
47/50

Fig.47



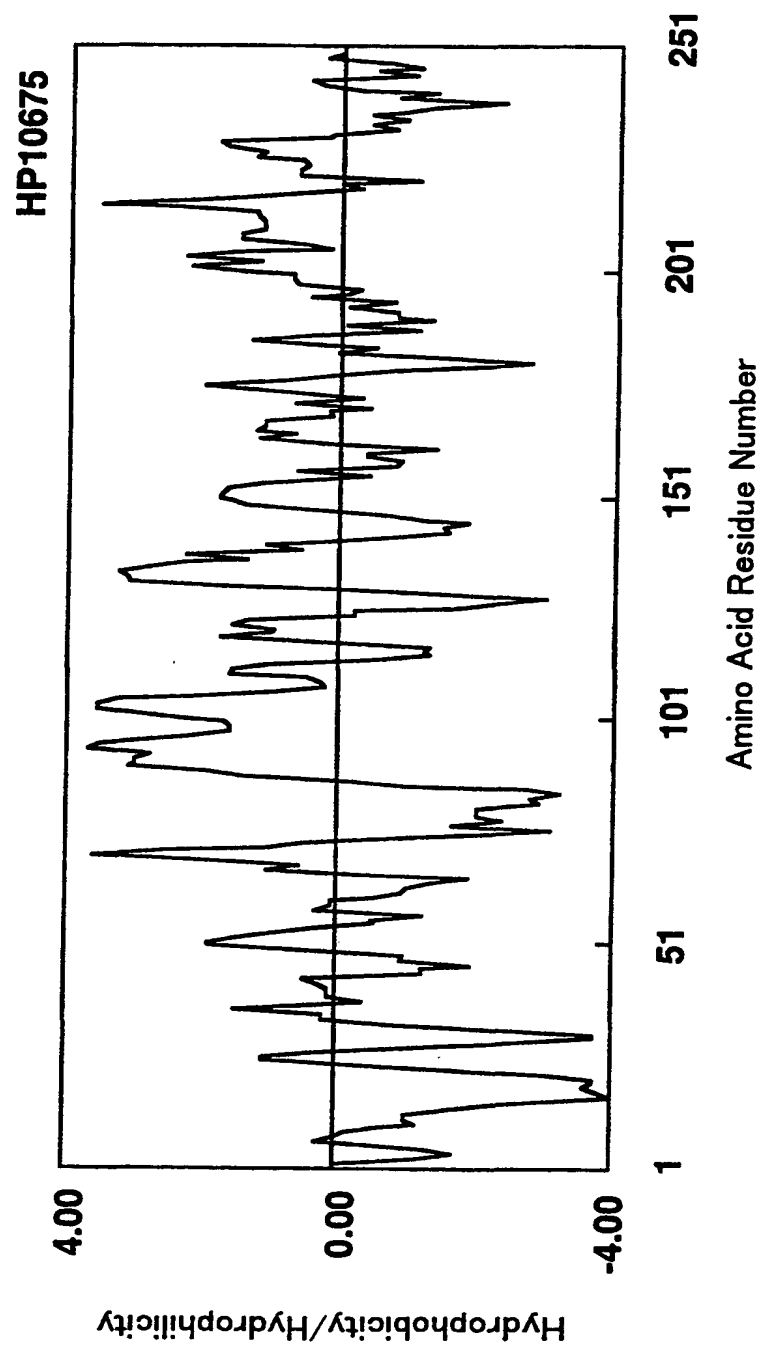
48/50

Fig.48



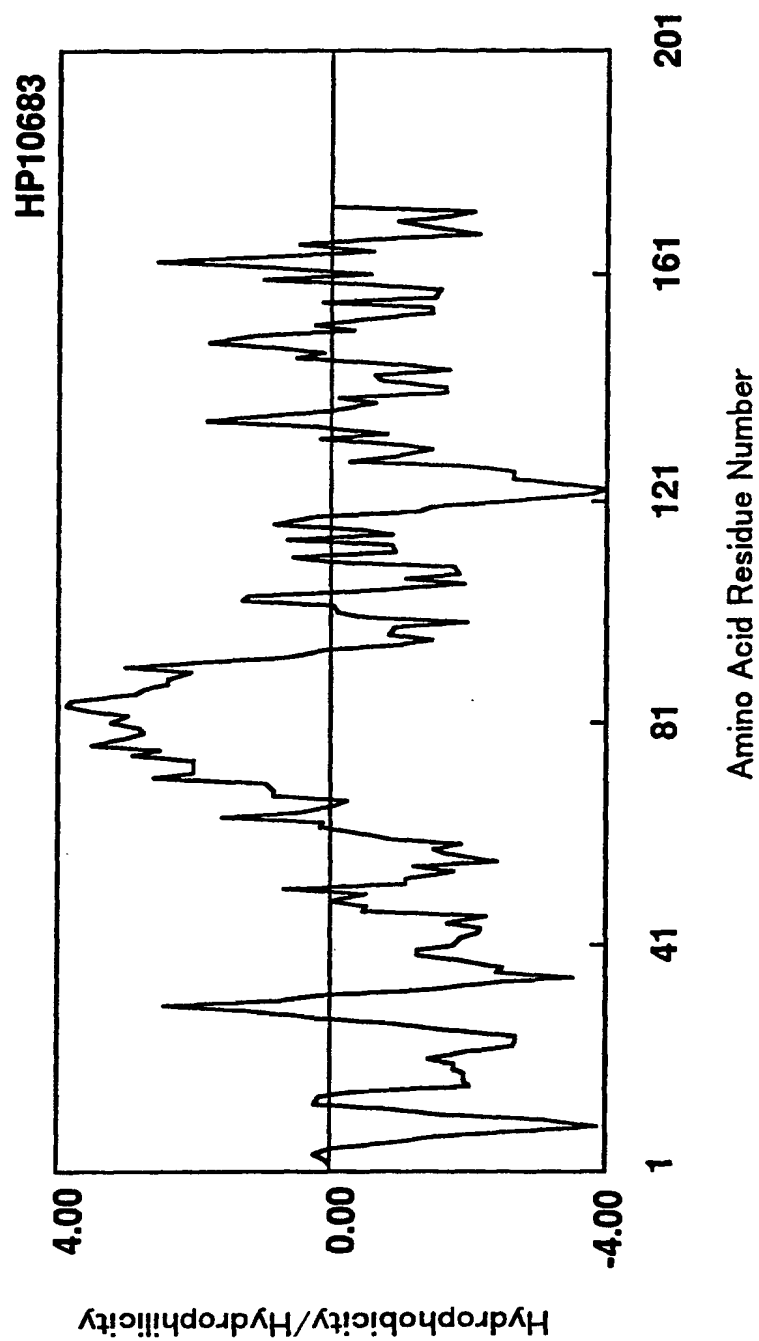
49/50

Fig.49



50/50

Fig.50



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SEQUENCE LISTING

<110> Sagami Chemical Research Center,
Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
proteins

<130> 661607

<150> JP 10-326255

<151> 1998-11-17

<150> JP 10-364315

<151> 1998-12-22

<150> JP 11-69811

<151> 1999-03-16

<150> JP 11-119299

<151> 1999-04-27

<150> JP 11-138169

<151> 1999-05-19

<160> 150

<210> 1

<211> 647

<212> PRT

<213> Homo sapiens

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1

5

10

15

Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu

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Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro		
35	40	45
Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Leu Trp Leu Leu Glu Ala		
50	55	60
Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly		
65	70	75
Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln		
85	90	95
Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp		
100	105	110
His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala		
115	120	125
Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu		
130	135	140
Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln		
145	150	155
Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val		
165	170	175
Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu		
180	185	190
Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln		
195	200	205
Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly		
210	215	220
Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro		
225	230	235
Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly		
245	250	255
Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly		
260	265	270
Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr		
275	280	285
His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys		
290	295	300

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Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg			
305	310	315	320
Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe			
325	330	335	
Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu			
340	345	350	
Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala			
355	360	365	
Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys			
370	375	380	
Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu			
385	390	395	400
Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser			
405	410	415	
Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly			
420	425	430	
Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His			
435	440	445	
Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala			
450	455	460	
Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly			
465	470	475	480
Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe			
485	490	495	
Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser			
500	505	510	
Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu			
515	520	525	
Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr			
530	535	540	
Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala			
545	550	555	560
Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser			
565	570	575	
Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro			

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Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro
 165 170 175
 Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met
 180 185 190
 Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu
 195 200 205
 Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly
 210 215 220
 Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly
 225 230 235 240
 Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg Cys
 245 250 255
 Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile Cys Lys
 260 265 270
 Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu Glu Thr
 275 280 285
 Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp His Pro Ala
 290 295 300
 Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu Pro Thr Ser
 305 310 315 320
 Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly Pro Ser Thr
 325 330 335
 Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu Val
 340 345 350

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<211> 206

<212> PRT

<213> Homo sapiens

<400> 3

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 1 5 10 15
 Val Val Tyr Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val
 20 25 30
 Phe Leu Leu Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn

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35	40	45
Lys Met Ala Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser		
50	55	60
Leu Asn Asp Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser		
65	70	75
Ser Gln Pro Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro		
85	90	95
Ser Gly Leu Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro		
100	105	110
Leu Pro His Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser		
115	120	125
Gly His Pro Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly		
130	135	140
Trp Lys Leu Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg		
145	150	155
Ala Leu Leu Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu		
165	170	175
Ala Trp Ala Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu		
180	185	190
Gly Pro Ser Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu		
195	200	205

<210> 4

<211> 213

<212> PRT

<213> Hmo sapiens

<400> 4

Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys		
1	5	10
Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val		
20	25	30
Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser		
35	40	45
Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val Val Leu		
50	55	60

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Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala Gly Cys
 65 70 75 80
 Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn Gln Cys
 85 90 95
 Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn
 100 105 110
 Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser
 115 120 125
 Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly
 130 135 140
 Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe
 145 150 155 160
 Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile
 165 170 175
 Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe
 180 185 190
 Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys
 195 200 205
 Ala Gly His His Phe
 210

<210> 5

<211> 595

<212> PRT

<213> Homo sapiens

<400> 5

Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu
 1 5 10 15
 Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala
 20 25 30
 Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
 35 40 45
 Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
 50 55 60
 Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu

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65	70	75	80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp			
85	90	95	
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys			
100	105	110	
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu			
115	120	125	
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala			
130	135	140	
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met			
145	150	155	160
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr			
165	170	175	
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg			
180	185	190	
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe			
195	200	205	
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu			
210	215	220	
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp			
225	230	235	240
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly			
245	250	255	
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val			
260	265	270	
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile			
275	280	285	
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser			
290	295	300	
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp			
305	310	315	320
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg			
325	330	335	
Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp			
340	345	350	

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Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
 355 360 365
 Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
 370 375 380
 Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
 385 390 395 400
 Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
 405 410 415
 Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
 420 425 430
 Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
 435 440 445
 Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
 450 455 460
 Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
 465 470 475 480
 Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
 485 490 495
 Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
 500 505 510
 Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
 565 570 575
 Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln Pro Arg
 580 585 590
 Asp Glu Leu
 595

<210> 6

<211> 264

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<212> PRT

<213> Homo sapiens

<400> 6

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  1             5             10             15
Ala Glu Leu Arg Glu Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu
      20             25             30
Cys Glu Ser Gly His Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr
      35             40             45
Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
      50             55             60
Ser Cys Cys Cys Ala Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln
      65             70             75             80
Gln Gln Gln Arg Gln Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala
      85             90             95
Cys His Gly Ala Gly Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg
      100            105            110
Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg
      115            120            125
Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu
      130            135            140
Thr Ala Ser Ser Glu Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro
      145            150            155            160
Ala His Phe Glu Gly Thr Asn Val Glu Gly Val Ser Ser His Gln Ser
      165            170            175
Ala Pro Pro His Gln Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala
      180            185            190
Ser Thr Pro Pro Ser Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly
      195            200            205
Ile Glu Leu Cys Pro Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys
      210            215            220
Glu Val Arg Val Ser Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro
      225            230            235            240
Cys Ala Leu Pro Pro Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu
      245            250            255

```

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Ser Ser Ser Glu Gly Asp Ile Pro

260

<210> 7

<211> 343

<212> PRT

<213> Homo sapiens

<400> 7

Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1

5

10

15

Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu

20

25

30

Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr

35

40

45

Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala

50

55

60

Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala

65

70

75

80

Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp

85

90

95

Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val

100

105

110

Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala

115

120

125

Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu

130

135

140

Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr

145

150

155

160

Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr

165

170

175

Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp

180

185

190

Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu

195

200

205

Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu

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210	215	220
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr		
225	230	235 240
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr		
245	250	255
Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu		
260	265	270
Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe		
275	280	285
Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu		
290	295	300
Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly		
305	310	315 320
Asn Phe Phe Thr Thr Leu Arg Val Val His His Lys Phe His Ser Gln		
325	330	335
Arg His Gly Ser Lys Lys Asp		
340		

<210> 8

<211> 244

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr		
1	5	10 15
Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys		
20	25	30
Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn		
35	40	45
Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly		
50	55	60
Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly		
65	70	75 80
Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys		
85	90	95

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Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala
 100 105 110
 Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu
 115 120 125
 Asp Met Arg Gln Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr
 130 135 140
 Leu Val Leu Cys Ser Val Gln Ser Pro Arg Lys Val Leu Gln Glu Val
 145 150 155 160
 Arg Arg Val Leu Arg Pro Gly Gly Val Leu Phe Phe Trp Glu His Val
 165 170 175
 Ala Glu Pro Tyr Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu
 180 185 190
 Pro Thr Trp Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr
 195 200 205
 Trp Lys Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg
 210 215 220
 Gln Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
 225 230 235 240
 Lys Ala Val Lys

<210> 9

<211> 303

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser
 1 5 10 15
 Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp
 20 25 30
 Cys Leu Pro Pro Leu Arg Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp
 35 40 45
 Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala
 50 55 60
 Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val

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65	70	75	80
Thr Pro Thr Tyr Ala Arg Pro Leu Trp Val Gln Tyr Pro Gln Asp Val			
85	90	95	
Thr Thr Phe Asn Ile Asp Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu			
100	105	110	
Val His Pro Val Ser Asp Ser Gly Ala His Gly Val Gln Val Tyr Leu			
115	120	125	
Pro Gly Gln Gly Glu Val Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His			
130	135	140	
His Gly Pro Gln Thr Leu Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro			
145	150	155	160
Val Phe Gln Arg Gly Gly Thr Ile Val Pro Arg Trp Met Arg Val Arg			
165	170	175	
Arg Ser Ser Glu Cys Met Lys Asp Asp Pro Ile Thr Leu Phe Val Ala			
180	185	190	
Leu Ser Pro Gln Gly Thr Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly			
195	200	205	
His Thr Phe Asn Tyr Gln Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe			
210	215	220	
Ser Phe Ser Gly Asn Thr Leu Val Ser Ser Ser Ala Asp Pro Glu Gly			
225	230	235	240
His Phe Glu Thr Pro Ile Trp Ile Glu Arg Val Val Ile Ile Gly Ala			
245	250	255	
Gly Lys Pro Ala Ala Val Val Leu Gln Thr Lys Gly Ser Pro Glu Ser			
260	265	270	
Arg Leu Ser Phe Gln His Asp Pro Glu Thr Ser Val Leu Val Leu Arg			
275	280	285	
Lys Pro Gly Ile Asn Val Ala Ser Asp Trp Ser Ile His Leu Arg			
290	295	300	

<210> 10

<211> 160

<212> PRT

<213> Homo sapiens

<400> 10

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Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
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 Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
 20 25 30
 Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
 35 40 45
 Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
 50 55 60
 Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
 65 70 75 80
 Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
 85 90 95
 Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
 100 105 110
 Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 115 120 125
 Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
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 Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys Leu Ala
 145 150 155 160

<210> 11

<211> 1941

<212> DNA

<213> Homo sapiens

<400> 11

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 tgttcgcgtg agctcaagtt ctctctgtgc tccatgtacg cgcccggtgt caccgtgcta 540

16/233

gagcaggcgc	tgccgccctg	ccgctccctg	tgcgagcgcg	cgcgccaggg	ctgcgaggcg	600
ctcatgaaca	agttcggctt	ccagtggcca	gacacgctca	agtgtgagaa	gttcccggtg	660
cacggcgccg	gcgagctgtg	cgtgggccag	aacacgtccg	acaagggcac	cccagcgccc	720
tcgctgcttc	cagagttctg	gaccagcaac	cctcagcacg	gcggcggagg	gcaccgtggc	780
ggcttcccgg	ggggcgccgg	cgcgtcggag	cgaggcaagt	tctcctgcc	gcgcgccctc	840
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gagccgacca	aggtgtatgg	gctcatgtac	ttcggggccc	aggagctgcg	cttctcgcgc	960
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tgccctcacc	tccaggcggg	cggaggcgcc	ccgccgcacc	cgcccatgag	cccggacttc	1800
acggtcttca	tgattaagta	ccttatgacg	ctgatcgtgg	gcatcacgtc	gggcttctgg	1860
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<210> 12

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 12

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cttccagctc	tgtttggggc	taccttgagc	caggagggcc	tccaggggtt	ccttggtggag	180
gctcaccacg	acaatgcctg	cagccccatt	gccccaccac	ccccagcccc	ggtcaatggg	240
tcagtcttta	ttgcgtgct	tcgaagattc	gactgcaact	ttgacctcaa	ggtcctaaat	300

17/233

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gcccagaagg ctggatatgg tgccgctgta gtacacaatg tgaattccaa tgaacttctg 360
aacatggtgt ggaatagtga ggaaatccag cagcagatct ggatcccgtc tgtattttatt 420
ggggagagaa gctccgagta cctgcgtgcc ctctttgtct acgagaaggg ggctcggggtg 480
cttctgggtc cagacaatac cttcccccttg ggctattacc tcatcccttt cacagggatt 540
gtgggactgc tggttttggc catgggagca gtaatgatag ctcgttgtat ccagcacccg 600
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gacaagctgc gggactccc ctgtgctcat gcctaccaca gccgctgcgt ggacccctgg 780
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gaccaccctg cctcagaaag gaccccaact ttgggtteta gcccactct tcccacctcc 960
tttggttct tagccccagc tccccttggt ttctctgggc cttcaacaga tcccactg 1020
tcccctcct cttccccctg tctcctggtc 1050

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<210> 13

<211> 618

<212> DNA

<213> Homo sapiens

<400> 13

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tttgtctcag tgtacaagat caacaaaatg gccttctggg tcggagagac agtgtttctc 180
ctctggaaca gcctcaatga cccctcttc ggttggtca gtgaccggca gttcctcagc 240
tcccagcccc ggggaagaga tctaccctgg cttggttgg ttggccctc tggactgtgg 300
actgcaaaca ccctctgctg cttctggaag attcctttgc cccatccctg cttgagcccg 360
tcatcaccac caaccttgag aagtgggcat ccataacct ttggccatca gcccaacagg 420
ctaataaggg ggtggaaatt ggggcagagg aggagagtgt acccactggt caggcgccgg 480
gctctcctca agggctgtgg tgctggcccg ggtgcaggcc ctgggctggc atgggcccgt 540
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gctgtgctg tgctctca 618

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<210> 14

<211> 639

<212> DNA

<213> Homo sapiens

18/233

<400> 14

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tggagcgaaa aggtgtgct gtccgacctc accaaagtga cccggatgca tggaaatcgac	180
cctgtggtgc tggctcctgat ggtgggcgtg gtgatgttca ccctgggggt cgccggctgc	240
gtgggggctc tgcgggagaa tatctgcttg ctcaacttta accagtgtg tggcgcatat	300
ggccctgaag actgggacct caacgtctac ttcaattgca gcgtgccag ctacagccga	360
gagaagtgcg gggccccctt ctctgctgc gtgccagatc ctgcgcaaaa agttgtgaac	420
acacagtgtg gatatgatgt caggattcag ctgaagagca agtgggatga gtccatcttc	480
acgaaaggct gcatccaggc gctggaaagc tggctccgc ggaacattta cattgtggct	540
ggcgtcttca tcgccatctc gctgttgag atatttgga tcttcctggc aaggacgctg	600
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<210> 15

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 15

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aatgccgaac actcgtgccc ccaactacct ggcgctctgg agcggtgga ctacccccgg	180
gccaggatgg ccctctggtg tgccacggac cacaatgtgg acaacaccac agagatgctg	240
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gagcccaggt tctaccaga tgaagagggc ccaagcact ggaccaaaga aaggcaccag	360
tttctgatgg agctgaagca ggaagccctc acctttgcca ggaactgggg ggccgactat	420
atcctgtttg cagacacaga caacattctg accaacaatc agactctgcg gcttctcatg	480
gggcaggggc ttccagtggg ggcccaatg ctggactccc agacctacta ctccaacttc	540
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aaccgccagc gccggggctg ctcccgctgc cccatggtcc actccacctt ccttgcatcc	660
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cctttcgacg acatcctcgt ctccgctat gcctgccagg ctgctggggg ctccgtccac	780
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atgcaggcct cagctcatgt gactcggccc tctaagaggc ccagcaagat agggtttgac	960
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19/233

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ggcgcactc tgaccaaggg cgaggtgggc tgettectca gccattactc catctgggaa 1200
gaggtggttg ccaggggcct ggcccgggtc ctggtgtttg aggatgacgt gcgctttgag 1260
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cgctcatca gctggagcgg ctccaaaag accctgcgca gccccgcct ggacctgact 1740
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<210> 16

<211> 792

<212> DNA

<213> Homo sapiens

<400> 16

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gagactgget gctgcacct ctactatgag ctctggtggt tctggetget ctggactgtc 180
ctcatcctct ttagctgctg ttgcgcctc cgccaccgac gagctaaact caggctgcaa 240
caacagcagc ggcagcgtga aatcaacttg ttggcctatc atggggcatg ccattggggt 300
ggtcctttcc ctaccggttc actgcttgac ctctgcttcc tcagcacctt caagccccc 360
gcctacgagg atgtggttca ccgccaggc acaccacccc ccccttatac tgtggcccc 420
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caggaggggt agcccggggc aggggtgacc cctgcctcca cccccccctc ctgcccgtat 600
cgccgtttaa ctggcgactc cgtattgag ctctgcccct gtctgcctc cgggtgagggt 660
gagccagtca aggaggtgag ggttagtgcc acctgccag atctggagga ctactcccc 720
tgtgcactac cccagagtc tgtaccgag atctttccca tggggctgtc ttccagtga 780
ggggacatcc ca 792

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<210> 17

20/233

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 17

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accaaacttc	agaacaattg	caccagctcc	atcacgcggc	agaagaagcg	gtccaggag	180
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caggagctgg	agaaccagat	gaaagagcgc	caaggcctct	tctttgacat	ggaggcctat	300
ttgcctaaga	agaatggatt	gtacctgagc	ctggttctgg	ggaacgtcaa	cgtcacgctc	360
ctgagcaagc	aggctaagtt	tgcctacaag	gacgagtatg	agaagttcaa	gctctacctc	420
accatcatcc	tcatcctcat	ctccttcaact	tgcgccttcc	tgtcaactc	cagggtgaca	480
gatgctgcct	tcaacttcct	gctgggtctgg	tactactgca	ccctgaccat	ccgggagagc	540
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accttcctgt	cgggagtc	gctgacgtgg	ccgacggtc	tcatgtacca	gaaattccgg	660
aaccaattcc	tctccttttc	catgtaccag	agcttcgtgc	agtttctcca	gtactactac	720
cagagcggct	gcctctaccg	cctgcggggc	ctgggcgagc	ggcacaccat	ggacctcaact	780
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aatttcttca	ccacctgag	ggttgtgcac	cacaagtttc	acagtcagcg	gcacgggagc	1020
aagaaggat						1029

<210> 18

<211> 732

<212> DNA

<213> Homo sapiens

<400> 18

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gccgtgctga	ctcccaagag	caaccgcaag	atggagagca	agaaacggga	gctcttcagc	180
cagataaagg	ggcttacagg	agcctccggg	aaagtggccc	tactggagct	gggctgcgga	240
accggagcca	actttcagtt	ctaccaccg	ggctgcaggg	tcacctgcct	agacccaaat	300
ccccactttg	agaagttcct	gacaaagagc	atggctgaga	acaggcacct	ccaatatgag	360
cgggtttgtg	tggctcctgg	agaggacatg	agacagctgg	ctgatggctc	catggatgtg	420

21/233

gtggtctgca ctctggtgct gtgctctgtg cagagcccaa ggaaggtcct gcaggaggtc 480
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 ggaagctggg ccttcatgtg gcagcaagtt ttcgagccca cctggaaaca cattggggat 600
 ggctgctgcc tcaccagaga gacctggaag gatcttgaga acgcccagtt ctccgaaatc 660
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<210> 19

<211> 909

<212> DNA

<213> Homo sapiens

<400> 19

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 gccgagcagc tacggcagaa ggatctgagg atttcccagc tgcaagcgga actccgacgg 180
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 taccagaagc atcatggtcc ccagaccctg tacctgcctg taactctaag cagtatccct 480
 gtgttccagc gtggaggggac aatcgtgcct cgatggatgc gagtggggcg gtcttcagaa 540
 tgtatgaagg atgaccccat cactctcttt gttgcactta gccctcaggg tacagctcaa 600
 ggagagctct ttctggatga tgggcacacg ttcaactatc agactcgcca agagttcctg 660
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 gctgtggtac tccagacaaa aggatctcca gaaagccgcc tgccttcca gcatgacct 840
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 cacctgca 909

<210> 20

<211> 480

<212> DNA

<213> Homo sapiens

<400> 20

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22/233

gaggttgttg aggcattcttc attaatctgg agtaccagga taaaaggctt cattgcgtgt 120
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 ggactacacc tcttcgcagt gttttatacc tttggtaata tcgcatcaat tgggagtacc 240
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 gcaactatca tgggtgctgtt gtgttttgca cttacctgt gttctgcctt ttggtggcat 360
 aacaagggac ttgcacttat cttctgcatt ttgcagtctt tggcattgac gtggtacagc 420
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<210> 21

<211> 4485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(2132)

<400> 21

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 gggagccgcc gccggcgtg cccctggcag cccagcgga gcggcgccaa gagaggagcc 180
 gagaaagt atg gct gag gag gag gcg cct aag aag tcc cgg gcc gcc gcc 230
 Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly
 1 5 10
 ggt gcc gcg agc tgg gaa ctt tgt gcc ggg gcg ctc tcg gcc cgg ctg 278
 Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu
 15 20 25 30
 acg gag gag gcc agc ggg gac gcc ggt gcc cgc cgc cgc ccg cca gtt 326
 Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val
 35 40 45
 gac ccc cgg cga ttg gcg cgc cag ctg ctg ctg ctg ctt tgg ctg ctg 374
 Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Leu Trp Leu Leu
 50 55 60
 gag gct ccg ctg ctg ctg ggg gtc cgg gcc cag gcg gcg gcc cag ggg 422
 Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly
 65 70 75
 cca gcc cag ggg ccc ggg ccg ggg cag caa ccg ccg ccg cct cag 470

23/233

Pro Gly Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln	
80 85 90	
cag caa cag agc ggg cag cag tac aac ggc gag cgg ggc atc tcc gtc	518
Gln Gln Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val	
95 100 105 110	
ccg gac cac ggc tat tgc cag ccc atc tcc atc ccg ctg tgc acg gac	566
Pro Asp His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp	
115 120 125	
atc gcg tac aac cag acc atc atg ccc aac ctg ctg ggc cac acg aac	614
Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn	
130 135 140	
cag gag gac gcg ggc ctg gag gtg cac cag ttc tac cct cta gtg aaa	662
Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys	
145 150 155	
gtg cag tgt tcc gct gag ctg aag ttc ttc ctg tgc tcc atg tac gcg	710
Val Gln Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala	
160 165 170	
ccc gtg tgc acc gtg cta gag cag gcg ctg ccg ccc tgc cgc tcc ctg	758
Pro Val Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu	
175 180 185 190	
tgc gag cgc gcg cgc cag ggc tgc gag gcg ctg atg aac aag ttc ggc	806
Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly	
195 200 205	
ttc cag tgg cca gac acg ctg aag tgt gag aag ttc ccg gtg cac ggc	854
Phe Gln Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly	
210 215 220	
gcc ggc gag ctg tgc gtg ggc cag aac acg tcc gac aag ggc acc ccg	902
Ala Gly Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro	
225 230 235	
acg ccc tcg ctg ctt cca gag ttc tgg acc agc aac cct cag cac ggc	950
Thr Pro Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly	
240 245 250	
ggc gga ggg cac cgt ggc ggc ttc ccg ggg ggc gcc ggc gcg tcg gag	998
Gly Gly Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu	
255 260 265 270	

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cga ggc aag ttc tcc tgc ccg cgc gcc ctc aag gtg ccc tcc tac ctc	1046
Arg Gly Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu	
275 280 285	
aac tac cac ttc ctg ggg gag aag gac tgc ggc gca cct tgt gag ccg	1094
Asn Tyr His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro	
290 295 300	
acc aag gtg tat ggg ctc atg tac ttc ggg ccc gag gag ctg cgc ttc	1142
Thr Lys Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe	
305 310 315	
tgc cgc acc tgg att ggc att tgg tca gtg ctg tgc tgc gcc tcc acg	1190
Ser Arg Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr	
320 325 330	
ctc ttc acg gtg ctt acg tac ctg gtg gac atg cgg cgc ttc agc tac	1238
Leu Phe Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr	
335 340 345 350	
ccg gag cgg ccc atc atc ttc ttg tcc ggc tgt tac acg gcc gtg gcc	1286
Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala	
355 360 365	
gtg gcc tac atc gcc ggc ttc ctc ctg gaa gac cga gtg gtg tgt aat	1334
Val Ala Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn	
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gac aag ttc gcc gag gac ggg gca cgc act gtg gcg cag ggc acc aag	1382
Asp Lys Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys	
385 390 395	
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Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met	
400 405 410	
gcc agc tcc atc tgg tgg gtg atc ctg tgc ctc acc tgg ttc ctg gcg	1478
Ala Ser Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala	
415 420 425 430	
gct ggc atg aag tgg ggc cac gag gcc atc gaa gcc aac tca cag tat	1526
Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr	
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Phe His Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile	

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Leu Ala Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe			
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gtg ggg ctt aac aac gtg gac gcg ctg cgt ggc ttc gtg ctg gcg ccc			1670
Val Gly Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro			
480	485	490	
ctc ttc gtg tac ctg ttt atc ggc acg tcc ttt ctg ctg gcc ggc ttt			1718
Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe			
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Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys			
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acc gag aag ctg gag aag ctc atg gtg cgc att ggc gtc ttc agc gtg			1814
Thr Glu Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val			
530	535	540	
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Leu Tyr Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu			
545	550	555	
cag gcc ttc cgg gac cag tgg gaa cgc agc tgg gtg gcc cag agc tgc			1910
Gln Ala Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys			
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Lys Ser Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala			
575	580	585	590
ccg ccg cac ccg ccc atg agc ccg gac ttc acg gtc ttc atg att aag			2006
Pro Pro His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys			
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tac ctt atg acg ctg atc gtg ggc atc acg tcg ggc ttc tgg atc tgg			2054
Tyr Leu Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp			
610	615	620	
tcc gcc aag acc ctc aac tcc tgg agg aag ttc tac acg agg ctc acc			2102
Ser Gly Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr			
625	630	635	
aac agc aaa caa ggg gag act aca gtc tgagaccgg ggctcagccc a			2150

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Asn Ser Lys Gln Gly Glu Thr Thr Val

640	645	
tgccagggcc	tcggccgggg	cgcagcgatc ccccaaagcc agcgccgtgg agttcgtgcc 2210
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actcagctcc	tgcaaaagct	tcctgcctcg agggaaaagg acacgagggc ccgactgcca 2330
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gaggaataga	agttttatata	tatataatac catattttta atttcacaaa taaaaaattc 4010
aaagttttgt	acaaaattat	atggattttg tgcctgaaaa taatagagct tgagctgtct 4070
gaactatttt	acatttttatg	gtgtctcata gccaatccca cagtgtaaaa attcaggaat 4130

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tcaatgaaaa aagtctaccc ttaaaccctc agatcagtct ttccaaagaa ttactctgtt 4190
 tgcattgttg tgattgacat ttgtgaagtc ccaagaaaag atctgttttc atgacagtag 4250
 aaaatagaag ttgcaaatt atttctttac tcaaagagga ttaaagaga actctaattt 4310
 taatattaaa gctttctttt ctttcagggg ataaatttac atgacttttt atattatgga 4370
 ggtttatatt taaatcatca cctttctcat attttttaga ggtattgtct tatctcttcc 4430
 ataatcttgg atattacaaa accctaaata ggcaatcaat aaatggttaa ctggc 4485

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<211> 1509

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<213> Homo sapiens

<220>

<221> CDS

<222> (253)...(1305)

<400> 22

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 agctgggaag tgggacctgg ggggtggttg acccctggga tcctaaagga ggggcaggga 180
 ggggcagaaa ctccgcttct gtccttgcct accaggacgc ggggcctcct cagcctcttt 240
 cctcccgctg cc atg cac cct gca gcc ttc ccg ctt cct gtg gtt gtg gcc 291
 Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala
 1 5 10
 gct gtg ctg tgg gga gcg gcc ccg acc cgg ggg ctc att cga gcg acc 339
 Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr
 15 20 25
 tcg gac cac aat gcc agc atg gac ttt gca gac ctt cca gct ctg ttt 387
 Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe
 30 35 40 45
 ggg gct acc ttg agc cag gag ggc ctc cag ggg ttc ctt gtg gag gct 435
 Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala
 50 55 60
 cac cca gac aat gcc tgc agc ccc att gcc cca cca ccc cca gcc ccg 483
 His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro
 65 70 75
 gtc aat ggg tca gtc ttt att gcg ctg ctt cga aga ttc gac tgc aac 531

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Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn	
80 85 90	
ttt gac ctc aag gtc cta aat gcc cag aag gct gga tat ggt gcc gct	579
Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala	
95 100 105	
gta gta cac aat gtg aat tcc aat gaa ctt ctg aac atg gtg tgg aat	627
Val Val His Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn	
110 115 120 125	
agt gag gaa atc cag cag cag atc tgg atc ccg tct gta ttt att ggg	675
Ser Glu Glu Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly	
130 135 140	
gag aga agc tcc gag tac ctg cgt gcc ctc ttt gtc tac gag aag ggg	723
Glu Arg Ser Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Glu Lys Gly	
145 150 155	
gct cgg gtg ctt ctg gtt cca gac aat acc ttc ccc ttg ggc tat tac	771
Ala Arg Val Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr	
160 165 170	
ctc atc cct ttc aca ggg att gtg gga ctg ctg gtt ttg gcc atg gga	819
Leu Ile Pro Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly	
175 180 185	
gca gta atg ata gct cgt tgt atc cag cac cgg aaa cgg ctc cag cgg	867
Ala Val Met Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg	
190 195 200 205	
aat cga ctt acc aaa gag caa ctg aaa cag att cct aca cat gac tat	915
Asn Arg Leu Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr	
210 215 220	
cag aag gga gac cag tat gat gtc tgt gcc att tgc ctg gat gaa tat	963
Gln Lys Gly Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr	
225 230 235	
gag gat ggg gac aag ctg cgg gta ctc ccc tgt gct cat gcc tac cac	1011
Glu Asp Gly Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His	
240 245 250	
agc cgc tgc gtg gac ccc tgg ctc act cag acc cgg aag acc tgc ccc	1059
Ser Arg Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro	
255 260 265	

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att tgc aag cag cct gtt cat cgg ggt cct ggg gac gaa gac caa gag      1107
Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu
270                275                280                285
gaa gaa act caa ggg caa gag gag ggt gat gaa ggg gag cca agg gac      1155
Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp
                290                295                300
cac cct gcc tca gaa agg acc cca ctt ttg ggt tct agc ccc act ctt      1203
His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu
                305                310                315
ccc acc tcc ttt ggt tcc tta gcc cca gct ccc ctt gtt ttt cct ggg      1251
Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly
                320                325                330
cct tca aca gat ccc cca ctg tcc cct ccc tct tcc cct gtt atc ctg      1299
Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu
                335                340                345
gtc taataacccc ccacacatac acctctggtg acctatttgc acagaccg      1350
Val
350
tcgtcttccc tccagtcttc tgagggatag gggacattcc atcccaagct tctcccttac      1410
ccacacctat ccttttgagg ggttttgggg tggggctggg gcaagcagag ggactgggtc      1470
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<211> 3059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (230)...(850)

<400> 23

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acaaggatat ttacctgctc ctacctgat ctagggacga ggatgggaag accgcctgtg      180
gccatgagcc ctccccggtg ctctggggc taaggctggg gctgcagcc atg ggg ctg      238
Met Gly Leu

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1

ggt cag ccc cag gcc tgg ttg ctg ggt ctg ccc aca gct gtg gtc tat	286
Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala Val Val Tyr	
5 10 15	
ggc tcc ctg gct ctc ttc acc acc atc ctg cac aat gtc ttc ctg ctc	334
Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val Phe Leu Leu	
20 25 30 35	
tac tat gtg gac acc ttt gtc tca gtg tac aag atc aac aaa atg gcc	382
Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn Lys Met Ala	
40 45 50	
ttc tgg gtc gga gag aca gtg ttt ctc ctc tgg aac agc ctc aat gac	430
Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser Leu Asn Asp	
55 60 65	
ccc ctc ttc ggt tgg ctc agt gac cgg cag ttc ctc agc tcc cag ccc	478
Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser Ser Gln Pro	
70 75 80	
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Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro Ser Gly Leu	
85 90 95	
tgg act gca aac acc ctc tgc tgc ttc tgg aag att cct ttg ccc cat	574
Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro Leu Pro His	
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Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly Trp Lys Leu	
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Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg Ala Leu Leu	
150 155 160	
aag ggc tgt ggt gct ggc ccg ggt gca ggc cct ggg ctg gca tgg gcc	766
Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu Ala Trp Ala	
165 170 175	
gct gct ggc gct gtc gtt cct ggc gtt ctg ggt gcc ctg ggc ccc agc	814

31/233

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 Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu
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<210> 24

<211> 2367

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(710)

<400> 24

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 Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp
 1 5 10
 tac aag tac ctc ctt ttc agc tac aac atc atc ttc tgg ttg gct gga 158
 Tyr Lys Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly
 15 20 25 30
 gtt gtc ttc ctt gga gtc ggg ctg tgg gca tgg agc gaa aag ggt gtg 206
 Val Val Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val
 35 40 45
 ctg tcc gac ctc acc aaa gtg acc cgg atg cat gga atc gac cct gtg 254
 Leu Ser Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val
 50 55 60
 gtg ctg gtc ctg atg gtg ggc gtg gtg atg ttc acc ctg ggg ttc gcc 302
 Val Leu Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala
 65 70 75
 ggc tgc gtg ggg gct ctg cgg gag aat atc tgc ttg ctc aac ttt aac 350
 Gly Cys Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn
 80 85 90

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Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro	
115 120 125	
ttc tcc tgc tgc gtg cca gat cct gcg caa aaa gtt gtg aac aca cag	494
Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln	
130 135 140	
tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag tcc	542
Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser	
145 150 155	
atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg cgg	590
Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg	
160 165 170	
aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg cag	638
Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln	
175 180 185 190	
ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag gca	686
Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala	
195 200 205	
gtg aag gcc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga gcc	740
Val Lys Ala Gly His His Phe	
210	
acgctgggag gccagagcct ttctctgcca tcagccctac gtccagaggg agaggagccg	800
acacccccag agccagtgcc ccattcttaag catcagcgtg acgtgacctc tctgtttctg	860
cttgctgggtg ctgaagacca aggggtcccc ttgttacctg cccaaacttg tgactgcac	920
cctctggagt ctacccagag acagagaatg tgtctttatg tgggagtggg gactctgaaa	980
gacagagagg gctcctgtgg ctgccaggag ggcttgactc agacccccctg cagctcaagc	1040
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ccacatctgt ggggtgggccg tgggtagagg gaccacaggg cgtggacagg gcattctctc	1160
ccatcaagca aagcagcatg ggggcctgcc cgtaacggga ggaggacgtg gccccgctgg	1220
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cctcagccat gttcaagtga agtaagcctg agccagtgcg tggactgggt ccacgggagt	1340
gccttgcca ctgtccccct gtgtccacca gctattctcc tggcgccgga actgcctctg	1400

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tgccatttgc ctctccccgg agacagcgt tctctgcaa ccacaccccg tgccatagca 1940
caaccccagg ctgcagctgc tcagaagctc caggcatttt gttctggtg accgccccta 2000
atgggatatc ggtgatcact ggtccacct tcctgtcagg gcttttctgg ggctgctctt 2060
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tggtgctact tctaacactt tgccatagct cagaccactt ctcacgttc agggatggac 2180
tgcaacctta atttacttgc cggagtgtac attctagtgt ggtgtatact ggtggctgtt 2240
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<400> 25

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1 5 10
ctg ctg ctc ctg ctg ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag 100
Leu Leu Leu Leu Leu Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu
15 20 25
tcg ccg ctg ccc gcc gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa 148
Ser Pro Leu Pro Ala Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu
30 35 40

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cac tgc ctg ccc cac tac ctg ggc gct ctg gag cgg ctg gac tac ccc	196
His Ser Leu Pro His Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro	
45 50 55	
cgg gcc agg atg gcc ctc tgg tgt gcc acg gac cac aat gtg gac aac	244
Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn	
60 65 70 75	
acc aca gag atg ctg cag gag tgg ctg gcg gct gtg ggc gat gac tat	292
Thr Thr Glu Met Leu Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr	
80 85 90	
gct gct gtg gtc tgg agg cct gag ggc gag ccc agg ttc tac cca gat	340
Ala Ala Val Val Trp Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp	
95 100 105	
gaa gag ggt ccc aag cac tgg acc aaa gaa agg cac cag ttt ctg atg	388
Glu Glu Gly Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met	
110 115 120	
gag ctg aag cag gaa gcc ctc acc ttt gcc agg aac tgg ggg gcc gac	436
Glu Leu Lys Gln Glu Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp	
125 130 135	
tat atc ctg ttt gca gac aca gac aac att ctg acc aac aat cag act	484
Tyr Ile Leu Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr	
140 145 150 155	
ctg cgg ctt ctc atg ggg cag ggg ctt cca gtg gtg gcc cca atg ctg	532
Leu Arg Leu Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu	
160 165 170	
gac tcc cag acc tac tac tcc aac ttc tgg tgt ggg atc acc ccc cag	580
Asp Ser Gln Thr Tyr Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln	
175 180 185	
ggc tac tac cgc cgc aca gcc gag tac ttc ccc acc aag aac cgc cag	628
Gly Tyr Tyr Arg Arg Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln	
190 195 200	
cgc cgg ggc tgc ttc cgt gtc ccc atg gtc cac tcc acc ttc ctt gca	676
Arg Arg Gly Cys Phe Arg Val Pro Met Val His Ser Thr Phe Leu Ala	
205 210 215	
tcc ctg cgg gct gaa ggg gca gac cag ctt gct ttc tac ccg cca cat	724
Ser Leu Arg Ala Glu Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His	

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ccc aac tac act tgg cct ttc gac gac atc atc gtc ttc gcc tat gcc				772
Pro Asn Tyr Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala				
	240	245	250	
tgc cag gct gct ggg gtc tcc gtc cac gtg tgc aat gag cac cgt tat				820
Cys Gln Ala Ala Gly Val Ser Val His Val Cys Asn Glu His Arg Tyr				
	255	260	265	
ggg tac atg aat gtg ccg gtg aaa tcc cac cag ggg ctg gaa gac gag				868
Gly Tyr Met Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu				
	270	275	280	
agg gtc aac ttc atc cac ctg atc tta gaa gca cta gtg gac ggc ccc				916
Arg Val Asn Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro				
	285	290	295	
cgc atg cag gcc tca gct cat gtg act cgg ccc tct aag agg ccc agc				964
Arg Met Gln Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser				
	300	305	310	315
aag ata ggg ttt gac gag gtc ttt gtc atc agc ctg gct cgc agg cct				1012
Lys Ile Gly Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro				
	320	325	330	
gac cgt cgg gaa cgc atg ctc gcc tcg ctc tgg gag atg gag atc tct				1060
Asp Arg Arg Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser				
	335	340	345	
ggg agg gtg gtg gac gct gtg gat ggc tgg atg ctc aac agc agt gcc				1108
Gly Arg Val Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala				
	350	355	360	
atc agg aac ctc ggc gta gac ctg ctc ccg ggc tac cag gac cct tac				1156
Ile Arg Asn Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr				
	365	370	375	
tcg ggc cgc act ctg acc aag ggc gag gtg ggc tgc ttc ctc agc cat				1204
Ser Gly Arg Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His				
	380	385	390	395
tac tcc atc tgg gaa gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg				1252
Tyr Ser Ile Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu				
	400	405	410	
gtg ttt gag gat gac gtg cgc ttt gag agc aac ttc agg ggg cgg ctg				1300

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Val Phe Glu Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu	
415 420 425	
gag cgg ctg atg gag gat gtg gag gca gag aaa ctg tct tgg gac ctg	1348
Glu Arg Leu Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu	
430 435 440	
atc tac ctc gga cgg aag cag gtg aac cct gag aag gag acg gcc gtg	1396
Ile Tyr Leu Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val	
445 450 455	
gag ggg ctg ccg ggc ctg gtg gtg gct ggg tac tcc tac tgg acg ctg	1444
Glu Gly Leu Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu	
460 465 470 475	
gcc tat gcc ctg cgt ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag	1492
Ala Tyr Ala Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln	
480 485 490	
cct ctg cgc cgc atg ctg ccc gtg gac gag ttc ctg ccc atc atg ttc	1540
Pro Leu Arg Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe	
495 500 505	
gac cag cac ccc aac gag cag tac aag gca cac ttc tgg cca cgg gac	1588
Asp Gln His Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp	
510 515 520	
ctg gtg gcc ttc tcc gcc cag ccc ctg ctc gct gcc cct acc cac tat	1636
Leu Val Ala Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr	
525 530 535	
gcc ggg gac gcc gag tgg ctc agt gac acg gag aca tcc tct cca tgg	1684
Ala Gly Asp Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp	
540 545 550 555	
gat gat gac agc ggc cgc ctc atc agc tgg agc ggc tcc caa aag acc	1732
Asp Asp Asp Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr	
560 565 570	
ctg cgc agc ccc cgc ctg gac ctg act ggc agc agc ggg cac agc ctc	1780
Leu Arg Ser Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu	
575 580 585	
caa ccc cag ccc cga gat gag ctc taggtccagg tgatgactgc aaagca	1830
Gln Pro Gln Pro Arg Asp Glu Leu	
590 595	

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gcagatcctg tcagacctgg ccaccacctt gggcatggcc actctgccct ctggacctgt 1950
ctttcatcgg gagaaaccac tcagagatgg atcccatcc ctaaaggtct cacagcaaag 2010
gagcaggact cccaggcccc tgtaccctgc ctggcctgat tcagggcctt gtggccccc 2070
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<213> Homo sapiens

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gca ggg acc atg gcg gtg gca gca gag ctt cga gag ctg tgc cca gga 101
Ala Gly Thr Met Ala Val Ala Ala Glu Leu Arg Glu Leu Cys Pro Gly
10 15 20 25
gtg aac aac cag ccc tac ctc tgt gag agt ggt cac tgc tgc ggg gag 149
Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His Cys Cys Gly Glu
30 35 40
act ggc tgc tgc acc tac tac tat gag ctc tgg tgg ttc tgg ctg ctc 197
Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
45 50 55
tgg act gtc ctc atc ctc ttt agc tgc tgt tgc gcc ttc cgc cac cga 245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
60 65 70
cga gct aaa ctc agg ctg caa caa cag cag cgg cag cgt gaa atc aac 293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln Arg Glu Ile Asn

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75	80	85	
ttg ttg gcc tat cat ggg gca tgc cat ggg gct ggt cct ttc cct acc			341
Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr			
90	95	100	105
ggt tca ctg ctt gac ctt cgc ttc ctc agc acc ttc aag ccc cca gcc			389
Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala			
110	115	120	
tac gag gat gtg gtt cac cgc cca ggc aca cca ccc ccc cct tat act			437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Pro Tyr Thr			
125	130	135	
gtg gcc cca ggc cgc ccc ttg act got tcc agt gaa caa acc tgc tgt			485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys			
140	145	150	
tcc tcc tca tcc agc tgc cct gcc cac ttt gaa gga aca aat gtg gaa			533
Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly Thr Asn Val Glu			
155	160	165	
ggt gtt tcc tcc cac cag agt gcc ccc ccc cat cag gag ggt gag ccc			581
Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Glu Gly Glu Pro			
170	175	180	185
ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc			629
Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser Cys Arg Tyr Arg			
190	195	200	
cgt tta act ggc gac tcc ggt att gag ctc tgc cct tgt cct gcc tcc			677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser			
205	210	215	
ggt gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca			725
Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser Ala Thr Leu Pro			
220	225	230	
gat ctg gag gac tac tcc ccg tgt gca cta ccc cca gag tct gta ccg			773
Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro			
235	240	245	
cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca			818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Ser Glu Gly Asp Ile Pro			
250	255	260	
ta agtagttttg agagggtgga tgggttactt gcccaccaga aacagcccta			870

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qcctttgatc tcattaaaga gatgtgaacc aget 1024

tactggctac tggcgctgca gcc atg cag ccc ccg ccc ccg ggc ccg ctg ggc	53
Met Gln Pro Pro Pro Pro Gly Pro Leu Gly	
1 5 10	
gac tgc ctg cgg gac tgg gag gat cta cag cag gac ttc cag aac atc	101
Asp Cys Leu Arg Asp Trp Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile	
15 20 25	
cag gag acc cat cgg ctc tac cgc ctg aag ctg gag gag ctg acc aaa	149
Gln Glu Thr His Arg Leu Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys	
30 35 40	
ctt cag aac aat tgc acc agc tcc atc acg cgg cag aag aag cgg ctc	197
Leu Gln Asn Asn Cys Thr Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu	
45 50 55	
cag gag ctg gcc ctc gcc ctg aag aaa tgc aaa ccc tcc ctc cca gca	245
Gln Glu Leu Ala Leu Ala Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala	
60 65 70	
gag gcc gag ggg gcc gca cag gag ctg gag aac cag atg aaa gag cgc	293
Glu Ala Glu Gly Ala Ala Gln Glu Leu Glu Asn Gln Met Lys Glu Arg	
75 80 85 90	
caa ggc ctc ttc ttt gac atg gag gcc tat ttg cct aag aag aat gga	341
Gln Gly Leu Phe Phe Asp Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly	
95 100 105	
ttg tac ctg agc ctg gtt ctg ggg aac gtc aac gtc acg ctc ctg agc	389
Leu Tyr Leu Ser Leu Val Leu Gly Asn Val Asn Val Thr Leu Leu Ser	

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Lys Gln Ala Lys Phe Ala Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu			
125	130	135	
tac ctc acc atc atc ctc atc ctc atc tcc ttc act tgc cgc ttc ctg			485
Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu			
140	145	150	
ctc aac tcc agg gtg aca gat gct gcc ttc aac ttc ctg ctg gtc tgg			533
Leu Asn Ser Arg Val Thr Asp Ala Ala Phe Asn Phe Leu Leu Val Trp			
155	160	165	170
tac tac tgc acc ctg acc atc cgg gag agc atc ctc atc aac aac ggc			581
Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly			
175	180	185	
tcc cgg atc aaa ggc tgg tgg gtg ttc cat cac tac gtg tcc acc ttc			629
Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe			
190	195	200	
ctg tcg gga gtc atg ctg acg tgg ccc gac ggt ctc atg tac cag aaa			677
Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys			
205	210	215	
ttc cgg aac caa ttc ctc tcc ttt tcc atg tac cag agc ttc gtg cag			725
Phe Arg Asn Gln Phe Leu Ser Phe Ser Met Tyr Gln Ser Phe Val Gln			
220	225	230	
ttt ctc cag tac tac tac cag agc ggc tgc ctc tac cgc ctg cgg gcg			773
Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala			
235	240	245	250
ctg ggc gag cgg cac acc atg gac ctc act gtg gag ggc ttc cag tcc			821
Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser			
255	260	265	
tgg atg tgg cgg ggc ctc acc ttc ctg ctg cct ttt ctt ttc ttt gga			869
Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly			
270	275	280	
cac ttc tgg cag ctt ttt aac gcg ctg acg ttg ttc aac ctg gcc cag			917
His Phe Trp Gln Leu Phe Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln			
285	290	295	
gac cct cag tgc aag gag tgg cag gtg ctt atg tgc ggc ttt ccc ttc			965

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 ctc ctc ctt ttc ctc ggc aat ttc ttc acc acc ctg agg gtt gtg cac 1013
 Leu Leu Leu Phe Leu Gly Asn Phe Phe Thr Thr Leu Arg Val Val His
 315 320 325 330
 cac aag ttt cac agt cag cgg cac ggg agc aag aag gat tgaggctg 1060
 His Lys Phe His Ser Gln Arg His Gly Ser Lys Lys Asp
 335 340
 ggccttcccc tgccggccca gaggggcttc tgtcctgtgt gttgtgggag gggatgggag 1120
 gcgcccctcg agtgtgcgtg taccaggggg tctcttctat tctcccttgg gttttatggg 1180
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 Met Asp Ile Leu Val Pro
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 Leu Leu Gln Leu Leu Val Leu Leu Leu Thr Leu Pro Leu His Leu Met
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 Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys Lys Ser Tyr Phe Pro Tyr
 25 30 35
 ctg atg gcc gtg ctg act ccc aag agc aac cgc aag atg gag agc aag 200
 Leu Met Ala Val Leu Thr Pro Lys Ser Asn Arg Lys Met Glu Ser Lys
 40 45 50
 aaa cgg gag ctc ttc agc cag ata aag ggg ctt aca gga gcc tcc ggg 248
 Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly
 55 60 65 70

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Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln	
75 80 85	
ttc tac cca ccg ggc tgc agg gtc acc tgc cta gac cca aat ccc cac	344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His	
90 95 100	
ttt gag aag ttc ctg aca aag agc atg gct gag aac agg cac ctc caa	392
Phe Glu Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln	
105 110 115	
tat gag egg ttt gtg gtg gct cct gga gag gac atg aga cag ctg gct	440
Tyr Glu Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala	
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gat ggc tcc atg gat gtg gtg gtc tgc act ctg gtg ctg tgc tct gtg	488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val	
135 140 145 150	
cag agc cca agg aag gtc ctg cag gag gtc cgg aga gta ctg aga ccg	536
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg Pro	
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Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr Gly Ser	
170 175 180	
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Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp Lys His Ile	
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200 205 210	
gcc cag ttc tcc gaa atc caa atg gaa cga cag ccc cct ccc ttg aag	728
Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln Pro Pro Pro Leu Lys	
215 220 225 230	
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Trp Leu Pro Val Gly Pro His Ile Met Gly Lys Ala Val Lys	
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44/233

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 tctccccact accaccttct tcctgagctg ggggcaccag ggagaatcag agatgctggg 1260
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 gacgaaacca cg 1332

<210> 29

<211> 1932

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38)...(949)

<400> 29

agaccccgcc tgctcgggcg cgggcggcgg cgcggcc atg aag ctg aag ctg aag 55
 Met Lys Leu Lys Leu Lys
 1 5
 aac gtg ttt ctc gcc tac ttc ctg gtg tgg atc gcc ggc ctc ctc tac 103
 Asn Val Phe Leu Ala Tyr Phe Leu Val Ser Ile Ala Gly Leu Leu Tyr
 10 15 20
 gcg ctg gta cag ctc ggc cag cca tgt gac tgc ctt cct ccc ctg cgg 151
 Ala Leu Val Gln Leu Gly Gln Pro Cys Asp Cys Leu Pro Pro Leu Arg
 25 30 35
 gca gca gcc gag cag cta cgg cag aag gat ctg agg att tcc cag ctg 199
 Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp Leu Arg Ile Ser Gln Leu
 40 45 50
 caa gcg gaa ctc cga cgg cca ccc cct gcc cct gcc cag ccc cct gaa 247
 Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala Pro Ala Gln Pro Pro Glu
 55 60 65 70
 ccc gag gcc ctg cct act atc tat gtt gtt acc ccc acc tat gcc agg 295
 Pro Glu Ala Leu Pro Thr Ile Tyr Val Val Thr Pro Thr Tyr Ala Arg
 75 80 85

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ccc ctg tgg gtg cag tac cct cag gat gtg act acc ttc aat ata gat	343
Pro Leu Trp Val Gln Tyr Pro Gln Asp Val Thr Thr Phe Asn Ile Asp	
90 95 100	
gat cag tac ttg ctt ggg gat gcg ttg ctg gtt cac cct gta tca gac	391
Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu Val His Pro Val Ser Asp	
105 110 115	
tct gga gcc cat ggt gtc cag gtc tat ctg cct ggc caa ggg gag gtg	439
Ser Gly Ala His Gly Val Gln Val Tyr Leu Pro Gly Gln Gly Glu Val	
120 125 130	
tgg tat gac att caa agc tac cag aag cat cat ggt ccc cag acc ctg	487
Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His His Gly Pro Gln Thr Leu	
135 140 145 150	
tac ctg cct gta act cta agc agt atc cct gtg ttc cag cgt gga ggg	535
Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro Val Phe Gln Arg Gly Gly	
155 160 165	
aca atc gtg cct cga tgg atg cga gtg cgg cgg tct tca gaa tgt atg	583
Thr Ile Val Pro Arg Trp Met Arg Val Arg Arg Ser Ser Glu Cys Met	
170 175 180	
aag gat gac ccc atc act ctc ttt gtt gca ctt agc cct cag ggt aca	631
Lys Asp Asp Pro Ile Thr Leu Phe Val Ala Leu Ser Pro Gln Gly Thr	
185 190 195	
gct caa gga gag ctc ttt ctg gat gat ggg cac acg ttc aac tat cag	679
Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly His Thr Phe Asn Tyr Gln	
200 205 210	
act cgc caa gag ttc ctg ctg cgt cga ttc tca ttc tct ggc aac acc	727
Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe Ser Phe Ser Gly Asn Thr	
215 220 225 230	
ctt gtc tcc agc tca gca gac cct gaa gga cac ttt gag aca cca atc	775
Leu Val Ser Ser Ser Ala Asp Pro Glu Gly His Phe Glu Thr Pro Ile	
235 240 245	
tgg att gag cgg gtg gtg ata ata ggg gct gga aag cca gca gct gtg	823
Trp Ile Glu Arg Val Val Ile Ile Gly Ala Gly Lys Pro Ala Ala Val	
250 255 260	
gta ctc cag aca aaa gga tct cca gaa agc cgc ctg tcc ttc cag cat	871
Val Leu Gln Thr Lys Gly Ser Pro Glu Ser Arg Leu Ser Phe Gln His	

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265	270	275	
gac cct gag acc tct gtg ttg gtc ctg cgc aag cct ggc atc aat gtg			919
Asp Pro Glu Thr Ser Val Leu Val Leu Arg Lys Pro Gly Ile Asn Val			
280	285	290	
gca tct gat tgg agt att cac ctg cga taacccaagg gatgttctgg gtta			970
Ala Ser Asp Trp Ser Ile His Leu Arg			
295	300		
gggggagggga aggggagcat tagtgetgag agatattcctt tcttctgcct tggagtctgg			1030
ccctccccag acttcaetta tgctagtcta agaccagat tctgccaaca tttgggcagg			1090
atgagagggc tgaccctggg ctccaaattc ctcttgtgat ctctcacct ctccactcc			1150
attgatacca actctttccc ttcattcccc caacatcctg ttgctctaac tggagcacat			1210
tcacttacga acaccaggaa accacagggc ccttgctgcc ccttctcttt cccttattta			1270
ggagccctga actccccag agtctatcca ttcattgcctc ttgtatgttg atgccacttc			1330
ttggaagaag atgagggcaa tgagttaggg ctcccttttcc ccttccctcc caccagattg			1390
ctctcccacc tttcatttct tctccaggc tttactcccc tttttatgcc ccaccgatac			1450
actgggacca ccccttacct cggacaggat gaatggatca aaggagttag gttgctaaag			1510
aacatccttt tccctctcat totacccttt tctctcccc gattccttgt agagctgctg			1570
caattcttag aggggcagtt ctacctctc tgctccctgg cagaaagacg tttccacacc			1630
tottagggga tgcgcattaa acttcttttg ccccttctt gtcccctttg aggggcactt			1690
aagatggaga aatcagttgt ggtttcagtg aatcatggtc acctgtattt attgctagga			1750
gaagcctgag ggtgggggga gatgatcatg tgtgctcggg gttggctgga agccctgggt			1810
gggggggttg gggaggacta atggggagtc ggggaatatt tgtgggtatt tttttactt			1870
cctcttggtt cccagctgtg acacgttttg atcaaaggag aaacaataaa gggataaacc			1930
at			1932

<210> 30

<211> 1124

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)...(555)

<400> 30

ggaagagccg tcaacttagc gagcgcaaca ggctgccgct gaggagctgg agctggtggg	60
gactggggccg ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac acg	111

47/233

Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr									
1	5	10							
gag gac cgg agc ggc ctg tcc gag gtt gtt gag gca tct tca tta agc			159						
Glu Asp Arg Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser									
15	20	25							
tgg agt acc agg ata aaa ggc ttc att gcg tgt ttt gct ata gga att			207						
Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile									
30	35	40	45						
ctc tgc tca ctg ctg ggt act gtt ctg ctg tgg gtg ccc agg aag gga			255						
Leu Cys Ser Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly									
50	55	60							
cta cac ctc ttc gca gtg ttt tat acc ttt ggt aat atc gca tca att			303						
Leu His Leu Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile									
65	70	75							
ggg agt acc atc ttc ctc atg gga cca gtg aaa cag ctg aag cga atg			351						
Gly Ser Thr Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met									
80	85	90							
ttt gag cct act cgt ttg att gca act atc atg gtg ctg ttg tgt ttt			399						
Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe									
95	100	105							
gca ctt acc ctg tgt tct gcc ttt tgg tgg cat aac aag gga ctt gca			447						
Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala									
110	115	120	125						
ctt atc ttc tgc att ttg cag tct ttg gca ttg acg tgg tac agc ctt			495						
Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu									
130	135	140							
tcc ttc ata cca ttt gca agg gat gct gtg aag aag tgt ttt gcc gtg			543						
Ser Phe Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val									
145	150	155							
tgt ctt gca taattcatgg ccagttttat gaagctttgg aaggcactat ggacagaa			600						
Cys Leu Ala									
160									
gctgggtggac agttttgtaa ctatcttcga aacctctgtc ttacagacat gtgcctttta			660						
tcttgacgca atgtgttgct tgtgattcga acatttgagg gttacttttg gaagcaacaa			720						
tacattctcg aacctgaatg tcagtagcac aggatgagaa gtgggttctg tatcttgtgg			780						

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agtggaatct tctcatgta cctgtttcct ctctggatgt tgtccactg aattcccatg      840
aatacaaacc tattcagcaa cagcacataa gccttggtg caagtgattc ccaggtggca      900
aaaggcagcc ccatcagaga tcacgggagc aacagtaagg gacagagttt tggggtccac      960
ttgtccctca gcatggaagc catcacctgt gtcctgcata gagtgagtct acttctactc     1020
tggcatctga gaacaagtga ctctgcttta gacaagcccc tggagagcct ggccatggag     1080
tgaggtagaa aagaagcact ttttggtggt atatgctgtt tctg                        1124

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<210> 31

<211> 1445

<212> PRT

<213> Homo sapiens

<400> 31

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Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys
  1              5              10              15
Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
      20              25              30
Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
      35              40              45
Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
      50              55              60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
      65              70              75              80
Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
      85              90              95
Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
      100             105             110
Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
      115             120             125
Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
      130             135             140
Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
      145             150             155             160
Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
      165             170             175
Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr

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180	185	190
Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val		
195	200	205
Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr		
210	215	220
Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser		
225	230	235
Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr		
245	250	255
Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser		
260	265	270
Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly		
275	280	285
Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp		
290	295	300
Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro		
305	310	315
Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg		
325	330	335
Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu		
340	345	350
Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala		
355	360	365
Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu		
370	375	380
Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu		
385	390	395
Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln		
405	410	415
Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe		
420	425	430
Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu		
435	440	445
Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser		
450	455	460

50/233

Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
 565 570 575
 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
 580 585 590
 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
 595 600 605
 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
 610 615 620
 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
 625 630 635 640
 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
 645 650 655
 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
 660 665 670
 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
 675 680 685
 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg
 690 695 700
 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
 705 710 715 720
 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
 725 730 735
 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu

51/233

740	745	750
Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile		
755	760	765
Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile		
770	775	780
Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn		
785	790	795
Ala Thr Gly His Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala		
805	810	815
Thr Val Leu Phe Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile		
820	825	830
Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met		
835	840	845
Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile		
850	855	860
Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu		
865	870	875
Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln		
885	890	895
Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala		
900	905	910
Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn		
915	920	925
Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln		
930	935	940
Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly		
945	950	955
Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala		
965	970	975
Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val		
980	985	990
Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn		
995	1000	1005
Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn		
1010	1015	1020

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Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
 1025 1030 1035 1040
 Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
 1045 1050 1055
 Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
 1220 1225 1230
 Ala Glu Leu Ala Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn
 1235 1240 1245
 Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
 1250 1255 1260
 Ala Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
 1265 1270 1275 1280
 Phe Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His
 1285 1290 1295
 Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly

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Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
 85 90 95
 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
 100 105 110
 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
 115 120 125
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
 130 135 140
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
 145 150 155 160
 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 165 170 175
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 180 185 190
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 195 200 205
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 210 215 220
 Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
 225 230 235 240
 Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val Phe His Val
 245 250 255
 Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln Leu Glu Thr
 260 265 270
 Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala Gly Asp Phe
 275 280 285
 Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr Leu Phe Asp
 290 295 300
 Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn Thr Tyr Ile Gly Gln Gly
 305 310 315 320
 Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala Cys Met Gly
 325 330 335
 Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr Gly Glu Asn
 340 345 350
 Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile Phe Asn Val

55/233

355	360	365
His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu Ile Arg Thr		
370	375	380
Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu Thr Thr Lys Leu Gly Asp		
385	390	395
Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly Thr Gln Leu		
405	410	415
Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr Leu Gly Ala		
420	425	430
Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly Met Cys Val		
435	440	445
Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala His Gly Glu		
450	455	460
Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu Phe Glu Val		
465	470	475
Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr Leu Phe Val		
485	490	495
Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Met Asp Leu Asn		
500	505	510
Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe Ile Lys Ala		
515	520	525
Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln Asp Pro Glu		
530	535	540
Lys Thr Ile Gly Asp Met Phe Gln Asn Gln Asp Arg Asn Gln Asp Gly		
545	550	555
Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu Asp Glu Glu		
565	570	575
Arg Val His Glu Glu Leu		
580		

<210> 33

<211> 410

<212> PRT

<213> Homo sapiens

<400> 33

56/233

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
 1 5 10 15
 Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
 20 25 30
 Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
 35 40 45
 Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
 50 55 60
 Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
 65 70 75 80
 Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
 85 90 95
 Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
 100 105 110
 Thr Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
 115 120 125
 Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
 130 135 140
 Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
 145 150 155 160
 Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
 165 170 175
 Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val
 180 185 190
 Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser
 195 200 205
 Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg
 210 215 220
 Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
 225 230 235 240
 Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
 245 250 255
 Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg
 260 265 270
 His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser

57/233

275	280	285
Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr Leu Ala Gln Arg Val		
290	295	300
Lys Glu Val Leu Pro His Val Pro Leu Gly Val Ile Gln Arg Asp Leu		
305	310	315
Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly		
325	330	335
Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu		
340	345	350
Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro		
355	360	365
Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu		
370	375	380
Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg		
385	390	395
Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp		
405	410	

<210> 34

<211> 483

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro		
1	5	10
Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg		
20	25	30
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro		
35	40	45
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp		
50	55	60
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile		
65	70	75
Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu Lys Asp Tyr Lys		
85	90	95

58/233

Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser
 100 105 110
 Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu Val Cys His Gly
 115 120 125
 Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile
 130 135 140
 Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu
 145 150 155 160
 Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile
 165 170 175
 Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly
 180 185 190
 Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser
 195 200 205
 Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu
 210 215 220
 Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr
 225 230 235 240
 Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val
 245 250 255
 Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu
 260 265 270
 Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe
 275 280 285
 Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe
 290 295 300
 Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr
 305 310 315 320
 Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys
 325 330 335
 Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp
 340 345 350
 Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp
 355 360 365
 Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu

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370 375 380
 Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu
 385 390 395 400
 Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly
 405 410 415
 Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val
 420 425 430
 Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr
 435 440 445
 Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro
 450 455 460
 Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser
 465 470 475 480
 Leu Pro Asn

<210> 35

<211> 607

<212> PRT

<213> Homo sapiens

<400> 35

Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly Gly Phe Gly Pro Phe
 1 5 10 15
 Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro Arg Val Leu Leu Pro
 20 25 30
 Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala Val Pro Ala His Arg
 35 40 45
 Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser His Gln Asp Val Trp
 50 55 60
 Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly Thr Leu Ser Ser Cys
 65 70 75 80
 Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn Thr Thr Leu Gly Glu
 85 90 95
 Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu Pro Ala Thr Val Pro
 100 105 110

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Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu Phe Ser Ser Thr Ile
 115 120 125
 Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile His Leu Glu Val Glu
 130 135 140
 Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala Gly Arg Gly Leu Pro
 145 150 155 160
 Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg Asp Lys Val Ser Tyr
 165 170 175
 Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu Leu Ser Gly Met Glu
 180 185 190
 Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn Arg Ala Ala Ser Thr
 195 200 205
 Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val Ala Phe Gly Tyr Leu
 210 215 220
 Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu Val Ala Tyr Val Ser
 225 230 235 240
 Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser Val Ser Tyr Val Met
 245 250 255
 Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala Leu Ala Gly Phe Thr
 260 265 270
 Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu Asp Val Glu His Arg
 275 280 285
 Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp Thr Gly Gly Val Met
 290 295 300
 Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp Trp Arg Trp Leu Leu
 305 310 315 320
 Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile Leu Ser Leu Trp Trp
 325 330 335
 Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln Gly His Val Lys Glu
 340 345 350
 Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu Asn Gly Arg Pro Val
 355 360 365
 Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser Lys Val Ala Ala Gly
 370 375 380
 Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp Leu Phe Arg Thr Pro

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385	390	395	400
Arg Leu Arg His Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val			
405	410	415	
Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu			
420	425	430	
Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser			
435	440	445	
Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr			
450	455	460	
Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu			
465	470	475	480
Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met			
485	490	495	
Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr			
500	505	510	
Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr			
515	520	525	
Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu			
530	535	540	
Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile			
545	550	555	560
Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu Pro Glu Thr Arg Gln			
565	570	575	
Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro			
580	585	590	
Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys Gln Val Gln Asn			
595	600	605	

<210> 36

<211> 314

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala

1

5

10

15

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Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
 20 25 30
 Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
 35 40 45
 Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
 50 55 60
 His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
 65 70 75 80
 Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
 85 90 95
 Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
 100 105 110
 Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
 115 120 125
 Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
 130 135 140
 Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
 145 150 155 160
 Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
 165 170 175
 Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
 180 185 190
 Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
 195 200 205
 Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
 210 215 220
 Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 225 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
 245 250 255
 Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
 260 265 270
 Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
 275 280 285
 Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu

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290 295 300
 Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

 <210> 37
 <211> 94
 <212> PRT
 <213> Homo sapiens
 <400> 37
 Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val
 1 5 10 15
 Met Val Val Ala Gly Val Val Val Leu Ile Leu Ala Leu Val Leu Ala
 20 25 30
 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly
 35 40 45
 Ala Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
 50 55 60
 Asp His Leu Val Ala Gly Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro
 65 70 75 80
 His Pro Ser Glu Ala Asn Thr Ser Leu Asp Lys Lys Ala Arg
 85 90

<210> 38
 <211> 218
 <212> PRT
 <213> Homo sapiens
 <400> 38
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
 1 5 10 15
 Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60

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Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln Arg Cys Trp
 115 120 125
 Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala Val His Arg
 130 135 140
 Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu Leu Thr Ala
 145 150 155 160
 Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser Pro Arg Arg
 165 170 175
 Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His Pro Gly Pro
 180 185 190
 Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro Asp Pro Gly
 195 200 205
 Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215

<210> 39

<211> 460

<212> PRT

<213> Homo sapiens

<400> 39

Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser
 1 5 10 15
 Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu
 20 25 30
 Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
 35 40 45
 Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
 50 55 60
 Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln

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65	70	75	80
Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu			
85	90	95	
Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu			
100	105	110	
Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu			
115	120	125	
Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln			
130	135	140	
Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu			
145	150	155	160
Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys			
165	170	175	
Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln			
180	185	190	
His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile			
195	200	205	
Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg			
210	215	220	
Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp			
225	230	235	240
Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr			
245	250	255	
Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val			
260	265	270	
Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg			
275	280	285	
Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr			
290	295	300	
Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile			
305	310	315	320
Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu			
325	330	335	
Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly			
340	345	350	

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Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
 435 440 445
 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40

<211> 216

<212> PRT

<213> Homo sapiens

<400> 40

Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu Leu
 1 5 10 15
 Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly Ile Lys
 20 25 30
 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro

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115	120	125
Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu Gln Arg Arg Met		
130	135	140
Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro		
145	150	155
Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser Thr Ala Pro Asp		
165	170	175
Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro		
180	185	190
Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe		
195	200	205
Tyr Glu Asp Asn Trp Ala Pro Pro		
210	215	

<210> 41

<211> 4335

<212> DNA

<213> Homo sapiens

<400> 41

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gccgtggctc ccgggcctcg gtttctggtg acagcccag ggatcatcag gcccgaggga	120
aatgtgacta ttgggtgga gcttctggaa cactgccctt cacaggtgac tgtgaaggcg	180
gagctgctca agacagcatc aaacctcact gtctctgtcc tggaagcaga aggagtcttt	240
gaaaaaggct cttttaagac acttactctt ccatcactac ctctgaacag tgcagatgag	300
atztatgagc tacgtgtaac cggacgtacc caggatgaga tttattctc taatagtacc	360
cgcttatcat ttgagaccaa gagaatatct gtcttcattc aaacagacaa ggccttatac	420
aagccaaagc aagaagtga gtttcgcatt gttacactct tctcagattt taagccttac	480
aaaacctctt taaacattct cattaaggac cccaaatcaa atttgatcca acagtgggtg	540
tcacaacaaa gtgatcttg agtcatttcc aaaacttttc agctatcttc ccatccaata	600
cttggtgact ggtctattca agttcaagt aatgaccaga catattatca atcatttcag	660
gtttcagaat atgtattacc aaaatttgaa gtgactttgc agacaccatt atattgttct	720
atgaattota agcattttaa tgggtaccatc acggcaaagt atacatatgg gaagccagtg	780
aaaggagacg taacgcttac atttttacct ttatcctttt ggggaaagaa gaaaaatatt	840
acaaaaacat ttaagataaa tggatctgca aacttctctt ttaatgatga agagatgaaa	900
aatgtaatgg attcttcaaa tggactttct gaatacctgg atctatcttt ccctggacca	960

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gtagaaat	ttt	taaccacagt	gacagaatca	gttacaggta	tttcaagaaa	tgtaagcact	1020
aatgtgttct	tcaagcaaca	tgattacatc	attgagtttt	ttgattatac	tactgtcttg		1080
aagccatctc	tcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg		1140
actcttgaag	aaagaagaaa	taatgtagtc	ataacagtga	cacagagaaa	ctatactgag		1200
tactggagcg	gatctaacag	tggaaatcag	aaaatggaag	ctgttcagaa	aataaattat		1260
actgtccccc	aaagtggaac	ttttaagatt	gaattcccaa	tcctggagga	ttccagtgag		1320
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aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga		1440
tcgccttttg	agttggtggt	tagtggcaac	aaacgattga	aggagttaag	ctatatggta		1500
gtatccaggg	gacagttggt	ggctgtagga	aaacaaaatt	caacaatgtt	ctctttaaca		1560
ccagaaaatt	cttggaactcc	aaaagcctgt	gtaattgtgt	attatattga	agatgatggg		1620
gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag		1680
ctatattgga	gtaaagtga	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg		1740
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gcctctaata	g	g	g	g	g		1860
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ttgacagatg	caaacctcac	gaaggattat	attgatgggtg	tttatgacaa	tgcaaatat		1980
gctgagaggt	ttatggagga	aaatgaagga	catattgtag	atattcatga	cttttctttg		2040
ggtagcagtc	cacatgtccg	aaagcatttt	ccagagactt	ggatttggct	agacaccaac		2100
atgggttcca	ggatttacca	agaatttgaa	gtaactgtac	ctgattctat	cacttcttgg		2160
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tcacaatcca	tcttattaga	cttgactgac	aataggctac	agagtaccct	gaaaactttg		2640
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tgtggtgaac	agaacatgat	aaattttgc	ccaaatattt	acattttgga	ttatctgact		2820
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gacccttctg	ggagcaactg	gttgtcagct	tttgttttaa	gatgtttcct	tgaagccgat		3000
ccttacatag	atattgatca	gaatgtgtta	cacagaacat	acacttggct	taaaggacat		3060

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cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gcttcaagggt 3120
 ggcaataaaa gtccagtaac acttacagcc tatattgtaa cttctctcct gggatataga 3180
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 ctgtcctcct gtgaccttg cagtgatgtc cagggtgcc gtccttgta ggatggagct 4260
 tcaggctccc atcatcactc ttcagtcatt tttattttct gtttcaagct tctgtacttt 4320
 atggaacttt ggctg 4335

<210> 42

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 42

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 ctactggtgg tgcaggccgt ggggaggggg ctgggccg ccagcccgcc cgggggcccc 120
 ctggaagatg tggatcatga gaggtaccac atccccagg cctgtccccg ggaagtgcag 180
 atgggggatt ttgtgcgcta ccaactacaac ggcacttttg aagatggcaa gaagtttgat 240
 tcaagctatg atcgcaacac cttggtggcc atcgtggtgg gtgtggggcg cctcatcact 300
 ggcattggacc gaggcctcat gggcatgtgt gtcaacgagc ggcgacgcct cattgtgcct 360
 cccacactgg gctatgggag catcggcctg ggggggctca ttccacggga tgccaccctc 420

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tacttcgatg tggttctgct ggatgtgtgg aacaaggaag acaccgtgca ggtgagcaca 480
 ttgctgcegc cgcctccactg ccccccgcag gtccaggacg gcgactttgt ccgctaccac 540
 tacaatggca ccctgctgga cggcacctcc ttcgacacca gctacagtaa gggcggcact 600
 tatgacacct acgtcggctc tggttggctg atcaagggca tggaccaggg gctgctgggc 660
 atgtgtcctg gagagagaag gaagattatc atccctccat tcctggccta tggcgagaaa 720
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 gagttctcca cttcatcaa ggctcaagtg agtgagggca aaggacgcct catgcctggg 1620
 caggacctg agaaaaccat aggagacatg ttccagaacc aggaccgcaa ccaggacggc 1680
 aagatcacag tcgacgagct caagctgaag tcagatgagg acgaggagcg ggtccacgag 1740
 gagctc 1746

<210> 43

<211> 1230

<212> DNA

<213> Homo sapiens

<400> 43

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 gactgcttcc tactgctcgt gctgctgctc tacgcgccag tcgggttctg cctcctcgtc 120
 ctgcgcctct ttctcgggat ccacgtcttc ctggtcagct gcgcgtgcc agacagcgtc 180
 cttcgcagat tcgtagtgcg gaccatgtgt gcggtgctag ggctcgtggc ccggcaggag 240
 gactccggac tccgggatca cagtgtcagg gtccctcattt ccaaccatgt gacaccttcc 300
 gaccacaaca tagtcaattt gcttaccacc tgtagcacc ctctactcaa tagtcccccc 360

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agctttgtgt gctggtctcg gggcttcatg gagatgaatg ggcgggggga gttggtggag 420
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gtgtcagatg cctcctgggt ctcagaactg ctgtgggtcac tttcgtccc tttcacgggtg 660
tatcaagtaa ggtggcttcg tcctgttcat cgccaactag ggggaagcga tgaggagttt 720
gcactccgtg tacaacagct ggtggccaag gaattggggc agacagggac acggctcact 780
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<210> 44

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 44

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ccactcttgt gcagtcatcc taaatatagg ttcagagcat ctctgtgaa tgacatattt 780
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<210> 45

<211> 1821

<212> DNA

<213> Homo sapiens

<400> 45

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ctggctgccc	tgcctgcccc	ccgatgtgcc	ctgccgggtg	cccctgcccc	cttcagccat	180
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cgtggggagc	tggaggatga	acctgccaca	gtgccctgct	ctcagggtcg	ggagtacgac	360
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ctggagggtg	aatgtcgggt	gaggcagctc	ccctggggagg	cagcaggctg	aggccttctc	480
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73/233

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 cccatgaagc aggtccagaa c 1821

<210> 46

<211> 942

<212> DNA

<213> Homo sapiens

<400> 46

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 cgcatcgtgg gtggagagga cgccgaactc gggcgcttggc cgtggcaggg gagcctgcgc 180
 ctgtgggatt cccacgtatg cggagtgagc ctgctcagcc accgctgggc actcacggcg 240
 ggcactgct ttgaaacct a tagtgacctt agtgatccct ccgggtggat ggtccagttt 300
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 gtgaagctgt ctgcacctgt cactacact aaacacatcc agcccatctg tctccaggcc 480
 tccacatttg agtttgagaa ccggacagac tgcctgggtga ctggctgggg gtacatcaaa 540
 gaggatgagg cactgccatc tccccacacc ctccaggaag ttcaggctgc catcataaac 600
 aactctatgt gcaaccacct cttcctcaag tacagtttcc gcaaggacat ctttgagagc 660
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 cccttggcct gtaacaagaa tggactgtgg tatcagattg gaggctgag ctggggagtg 780
 ggctgtggtc ggcccaatcg gcccggtgtc tacaccaata tcagccacca ctttgagtg 840
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<210> 47

<211> 282

<212> DNA

<213> Homo sapiens

<400> 47

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agcggtagca	accagctcct	gggcgctatt	gtgtcagcag	gcgacacatc	cgtcctccac	180
ctggggcatg	tggaccacct	ggtggcaggc	caaggcaacc	ccgagccaac	tgaactcccc	240
catccatcag	aggcaaatac	ttccctggac	aagaaagcca	ga		282

<210> 48

<211> 654

<212> DNA

<213> Homo sapiens

<400> 48

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gcagccgtgc	tgtgcgctag	tttcatgtcc	tttggcgtag	agcggcgctg	gttcgcgctg	240
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tcttgtgttg	gccagcgggtg	ctggggagct	gtaccgccgg	aaacctcgca	gccgtccct	420
gcagtccacc	ggccagggtg	tcctgggtat	ctacctcacc	tgtgtggcct	actcactgca	480
gcacagcaag	gaggaccggc	tggcgtatct	gaaccatctc	ccaggagggg	agctgatgat	540
ccagctgttc	ttcgtgctgt	atggcatcct	ggccctggcc	tttctgtcag	gctactacgt	600
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<210> 49

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 49

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caagacaatt catcatttga ttctctatct ccagagccaa aatcaagatt tgctatgta	120
gacgatgtaa aaattttagc caatggcctc cttcagttgg gacatggtct taaagacttt	180
gtccataaga cgaagggcca aattaatgac atattttcaaa aactcaacat atttgatcag	240
tctttttatg atctatcgct gcaaaccagt gaaatcaaag aagaagaaaa ggaactgaga	300
agaactacat ataaactaca agtcaaaaaat gaagaggtaa agaatatgtc acttgaactc	360
aactcaaaac ttgaaagcct cctagaagaa aaaattctac ttcaacaaaa agtgaaatat	420
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gtaacttcac ttaaaacttt tgtagaaaaa caagataata gcatcaaaga ccttctccag	540
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aatcagctca gaaggactag tattcaagaa cccacagaaa tttctctatc ttccaagcca	660
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gccatcagac ccagcaactc tcaagttttt catgtctact gtgatgttat atcaggtagt	840
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agagcaaaat ctaagccaga gaggagaaga ggattatctt ggaagtctca aaatggaagg	1320
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<210> 50

<211> 648

<212> DNA

<213> Homo sapiens

<400> 50

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tccttcctac tggggctggc tttgctgggc ataaagacgg acatcacccc cgttgcttat	120
ttctttctca cattgggtgg cttcttcttg tttgcctatc tctgggtccg gtttctggaa	180
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gcacgggaca atgaagcctt tgaagtgcc gtctatgaag aggccgtggt gggactagaa	300
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<210> 51

<211> 4473

<212> DNA

<213> Homo sapiens

<220>

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<400> 51

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1

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 Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys Thr Ala Ala Leu
 5 10 15 20

gcc gtg gct ccc ggg cct cgg ttt ctg gtg aca gcc cca ggg atc atc 152
 Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala Pro Gly Ile Ile
 25 30 35

agg ccc gga gga aat gtg act att ggg gtg gag ctt ctg gaa cac tgc 200
 Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys
 40 45 50

cct tca cag gtg act gtg aag gcg gag ctg ctg aag aca gca tca aac 248
 Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys Thr Ala Ser Asn
 55 60 65

ctc act gtc tct gtc ctg gaa gca gaa gga gtc ttt gaa aaa ggc tct 296
 Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe Glu Lys Gly Ser
 70 75 80

ttt aag aca ctt act ctt cca tca cta cct ctg aac agt gca gat gag 344
 Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu
 85 90 95 100

att tat gag cta cgt gta acc gga cgt acc cag gat gag att tta ttc 392

77/233

Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp Glu Ile Leu Phe	
105 110 115	
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Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg Ile Ser Val Phe	
120 125 130	
att caa aca gac aag gcc tta tac aag cca aag caa gaa gtg aag ttt	488
Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln Glu Val Lys Phe	
135 140 145	
cgc att gtt aca ctc ttc tca gat ttt aag cct tac aaa acc tct tta	536
Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr Lys Thr Ser Leu	
150 155 160	
aac att ctc att aag gac ccc aaa tca aat ttg atc caa cag tgg ttg	584
Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile Gln Gln Trp Leu	
165 170 175 180	
tca caa caa agt gat ctt gga gtc att tcc aaa act ttt cag cta tct	632
Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr Phe Gln Leu Ser	
185 190 195	
tcc cat cca ata ctt ggt gac tgg tct att caa gtt caa gtg aat gac	680
Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val Gln Val Asn Asp	
200 205 210	
cag aca tat tat caa tca ttt cag gtt tca gaa tat gta tta cca aaa	728
Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr Val Leu Pro Lys	
215 220 225	
ttt gaa gtg act ttg cag aca cca tta tat tgt tct atg aat tct aag	776
Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser Met Asn Ser Lys	
230 235 240	
cat tta aat ggt acc atc acg gca aag tat aca tat ggg aag cca gtg	824
His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr Gly Lys Pro Val	
245 250 255 260	
aaa gga gac gta acg ctt aca ttt tta cct tta tcc ttt tgg gga aag	872
Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser Phe Trp Gly Lys	
265 270 275	
aag aaa aat att aca aaa aca ttt aag ata aat gga tct gca aac ttc	920
Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly Ser Ala Asn Phe	
280 285 290	

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tct ttt aat gat gaa gag atg aaa aat gta atg gat tct tca aat gga	968
Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp Ser Ser Asn Gly	
295 300 305	
ctt tct gaa tac ctg gat cta tct ttc cct gga cca gta gaa att tta	1016
Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro Val Glu Ile Leu	
310 315 320	
acc aca gtg aca gaa tca gtt aca ggt att tca aga aat gta agc act	1064
Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg Asn Val Ser Thr	
325 330 335 340	
aat gtg ttc ttc aag caa cat gat tac atc att gag ttt ttt gat tat	1112
Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu Phe Phe Asp Tyr	
345 350 355	
act act gtc ttg aag cca tct ctc aac ttc aca gcc act gtg aag gta	1160
Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala Thr Val Lys Val	
360 365 370	
act cgt gct gat ggc aac caa ctg act ctt gaa gaa aga aga aat aat	1208
Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu Arg Arg Asn Asn	
375 380 385	
gta gtc ata aca gtg aca cag aga aac tat act gag tac tgg agc gga	1256
Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu Tyr Trp Ser Gly	
390 395 400	
tct aac agt gga aat cag aaa atg gaa gct gtt cag aaa ata aat tat	1304
Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln Lys Ile Asn Tyr	
405 410 415 420	
act gtc ccc caa agt gga act ttt aag att gaa ttc cca atc ctg gag	1352
Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe Pro Ile Leu Glu	
425 430 435	
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Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu Gly Ser Lys Ser	
440 445 450	
agc atg gca gtt cat agt ctg ttt aag tct cct agt aag aca tac atc	1448
Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser Lys Thr Tyr Ile	
455 460 465	
caa cta aaa aca aga gat gaa aat ata aag gtg gga tcg cct ttt gag	1496
Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly Ser Pro Phe Glu	

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470	475	480	
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Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu Ser Tyr Met Val			
485	490	495	500
gta tcc agg gga cag ttg gtg gct gta gga aaa caa aat tca aca atg			1592
Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln Asn Ser Thr Met			
505	510	515	
ttc tct tta aca cca gaa aat tct tgg act cca aaa gcc tgt gta att			1640
Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys Ala Cys Val Ile			
520	525	530	
gtg tat tat att gaa gat gat ggg gaa att ata agt gat gtt cta aaa			1688
Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser Asp Val Leu Lys			
535	540	545	
att cct gtt cag ctt gtt ttt aaa aat aag ata aag cta tat tgg agt			1736
Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys Leu Tyr Trp Ser			
550	555	560	
aaa gtg aaa gct gaa cca tct gag aaa gtc tct ctt agg atc tct gtg			1784
Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu Arg Ile Ser Val			
565	570	575	580
aca cag cct gac tcc ata gtt ggg att gta gct gtt gac aaa agt gtg			1832
Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val Asp Lys Ser Val			
585	590	595	
aat ctg atg aat gcc tct aat gat att aca atg gaa aat gtg gtc cat			1880
Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu Asn Val Val His			
600	605	610	
gag ttg gaa ctt tat aac aca gga tat tat tta ggc atg ttc atg aat			1928
Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly Met Phe Met Asn			
615	620	625	
tct ttt gca gtc ttt cag gaa tgt gga ctc tgg gta ttg aca gat gca			1976
Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val Leu Thr Asp Ala			
630	635	640	
aac ctc acg aag gat tat att gat ggt gtt tat gac aat gca gaa tat			2024
Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp Asn Ala Glu Tyr			
645	650	655	660
gct gag agg ttt atg gag gaa aat gaa gga cat att gta gat att cat			2072

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Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile Val Asp Ile His	
665 670 675	
gac ttt tct ttg ggt agc agt cca cat gtc cga aag cat ttt cca gag	2120
Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys His Phe Pro Glu	
680 685 690	
act tgg att tgg cta gac acc aac atg ggt tcc agg att tac caa gaa	2168
Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg Ile Tyr Gln Glu	
695 700 705	
ttt gaa gta act gta cct gat tct atc act tct tgg gtg gct act ggt	2216
Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp Val Ala Thr Gly	
710 715 720	
ttt gtg atc tct gag gac ctg ggt ctt gga cta aca act act cca gtg	2264
Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr Thr Thr Pro Val	
725 730 735 740	
gag ctc caa gcc ttc caa cca ttt ttc att ttt ttg aat ctt ccc tac	2312
Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu Asn Leu Pro Tyr	
745 750 755	
tct gtt atc aga ggt gaa gaa ttt gct ttg gaa ata act ata ttc aat	2360
Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile Thr Ile Phe Asn	
760 765 770	
tat ttg aaa gat gcc act gag gtt aag gta atc att gag aaa agt gac	2408
Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile Glu Lys Ser Asp	
775 780 785	
aaa ttt gat att cta atg act tca agt gaa ata aat gcc aca ggc cac	2456
Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn Ala Thr Gly His	
790 795 800	
cag cag acc ctt ctg gtt ccc agt gag gat ggg gca act gtt ctt ttt	2504
Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala Thr Val Leu Phe	
805 810 815 820	
ccc atc agg cca aca cat ctg gga gaa att cct atc aca gtc aca gct	2552
Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile Thr Val Thr Ala	
825 830 835	
ctt tca ccc act gct tct gat gct atc acc cag atg att tta gta aag	2600
Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met Ile Leu Val Lys	
840 845 850	

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gct gaa gga ata gaa aaa tca tat tca caa tcc atc tta tta gac ttg	2648
Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile Leu Leu Asp Leu	
855 860 865	
act gac aat agg cta cag agt acc ctg aaa act ttg agt ttc tca ttt	2696
Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu Ser Phe Ser Phe	
870 875 880	
cct cct aat aca gtg act ggc agt gaa aga gtt cag atc act gca att	2744
Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln Ile Thr Ala Ile	
885 890 895 900	
gga gat gtt ctt ggt cct tcc atc aat ggc tta gcc tca ttg att cgg	2792
Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala Ser Leu Ile Arg	
905 910 915	
atg cct tat ggc tgt ggt gaa cag aac atg ata aat ttt gct cca aat	2840
Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn Phe Ala Pro Asn	
920 925 930	
att tac att ttg gat tat ctg act aaa aag aaa caa ctg aca gat aat	2888
Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln Leu Thr Asp Asn	
935 940 945	
ttg aaa gaa aaa gct ctt tca ttt atg agg caa ggt tac cag aga gaa	2936
Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly Tyr Gln Arg Glu	
950 955 960	
ctt ctc tat cag agg gaa gat ggc tct ttc agt gct ttt ggg aat tat	2984
Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala Phe Gly Asn Tyr	
965 970 975 980	
gac cct tct ggg agc act tgg ttg tca gct ttt gtt tta aga tgt ttc	3032
Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val Leu Arg Cys Phe	
985 990 995	
ctt gaa gcc gat cct tac ata gat att gat cag aat gtg tta cac aga	3080
Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn Val Leu His Arg	
1000 1005 1010	
aca tac act tgg ctt aaa gga cat cag aaa tcc aac ggt gaa ttt tgg	3128
Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn Gly Glu Phe Trp	
1015 1020 1025	
gat cca gga aga gtg att cat agt gag ctt caa ggt ggc aat aaa agt	3176
Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly Gly Asn Lys Ser	

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1030	1035	1040	
cca gta aca ctt aca gcc tat att gta act tct ctc ctg gga tat aga			3224
Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu Leu Gly Tyr Arg			
1045	1050	1055	1060
aag tat cag cct aac att gat gtg caa gag tct atc cat ttt ttg gag			3272
Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile His Phe Leu Glu			
1065	1070	1075	
tct gaa ttc agt aga gga att tca gac aat tat act cta gcc ctt ata			3320
Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr Leu Ala Leu Ile			
1080	1085	1090	
act tat gca ttg tca tca gtg ggg agt cct aaa gcg aag gaa gct ttg			3368
Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala Lys Glu Ala Leu			
1095	1100	1105	
aat atg ctg act tgg aga gca gaa caa gaa ggt ggc atg caa ttc tgg			3416
Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly Met Gln Phe Trp			
1110	1115	1120	
gtg tca tca gag tcc aaa ctt tct gac tcc tgg cag cca cgc tcc ctg			3464
Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln Pro Arg Ser Leu			
1125	1130	1135	1140
gat att gaa gtt gca gcc tat gca ctg ctc tca cac ttc tta caa ttt			3512
Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His Phe Leu Gln Phe			
1145	1150	1155	
cag act tct gag gga atc cca att atg agg tgg cta agc agg caa aga			3560
Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu Ser Arg Gln Arg			
1160	1165	1170	
aat agc ttg ggt ggt ttt gca tct act cag gat acc act gtg gct tta			3608
Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr Thr Val Ala Leu			
1175	1180	1185	
aag gct ctg tct gaa ttt gca gcc cta atg aat aca gaa agg aca aat			3656
Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr Glu Arg Thr Asn			
1190	1195	1200	
atc caa gtg acc gtg acg ggg cct agc tca cca agt cct gta aag ttt			3704
Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser Pro Val Lys Phe			
1205	1210	1215	1220
ctg att gac aca cac aac cgc tta ctc ctt cag aca gca gag ctt gct			3752

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Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr Ala Glu Leu Ala	
1225 1230 1235	
gtg gta cag cca acg gca gtt aat att tcc gca aat ggt ttt gga ttt	3800
Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn Gly Phe Gly Phe	
1240 1245 1250	
gct att tgt cag ctc aat gtt gta tat aat gtg aag gct tct ggg tct	3848
Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys Ala Ser Gly Ser	
1255 1260 1265	
tct aga aga cga aga tct atc caa aat caa gaa gcc ttt gat tta gat	3896
Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala Phe Asp Leu Asp	
1270 1275 1280	
gtt gct gta aaa gaa aat aaa gat gat ctc aat cat gtg gat ttg aat	3944
Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His Val Asp Leu Asn	
1285 1290 1295 1300	
gtg tgt aca agc ttt tcg ggc ccg ggt agg agt ggc atg gct ctt atg	3992
Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly Met Ala Leu Met	
1305 1310 1315	
gaa gtt aac cta tta agt ggc ttt atg gtg cct tca gaa gca att tct	4040
Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser Glu Ala Ile Ser	
1320 1325 1330	
ctg agc gag aca gtg aag aaa gtg gaa tat gat cat gga aaa ctc aac	4088
Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His Gly Lys Leu Asn	
1335 1340 1345	
ctc tat tta gat tct gta aat gaa acc cag ttt tgt gtt aat att cct	4136
Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys Val Asn Ile Pro	
1350 1355 1360	
gct gtg aga aac ttt aaa gtt tca aat acc caa gat gct tca gtg tcc	4184
Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp Ala Ser Val Ser	
1365 1370 1375 1380	
ata gtg gat tac tat gag cca agg aga cag gcg gtg aga agt tac aac	4232
Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val Arg Ser Tyr Asn	
1385 1390 1395	
tct gaa gtg aag ctg tcc tcc tgt gac ott tgc agt gat gtc cag ggc	4280
Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser Asp Val Gln Gly	
1400 1405 1410	

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tgc cgt cct tgt gag gat gga gct tca ggc tcc cat cat cac tct tca 4328
 Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His His His Ser Ser
 1415 1420 1425
 gtc att ttt att ttc tgt ttc aag ctt ctg tac ttt atg gaa ctt tgg 4376
 Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe Met Glu Leu Trp
 1430 1435 1440
 ctg tgatttattt ttaaaggact ctgtgtaaca ctaacatttc cagtagtcac a 4430
 Leu
 1445
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 Met Phe Pro Ala Gly Pro Pro Ser His Ser
 1 5 10
 ctc ctc cgg ctc ccc ctg ctg cag ttg ctg cta ctg gtg gtg cag gcc 159
 Leu Leu Arg Leu Pro Leu Leu Gln Leu Leu Leu Leu Val Val Gln Ala
 15 20 25
 gtg ggg agg ggg ctg ggc cgc gcc agc ccg gcc ggg ggc ccc ctg gaa 207
 Val Gly Arg Gly Leu Gly Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu
 30 35 40
 gat gtg gtc atc gag agg tac cac atc ccc agg gcc tgt ccc cgg gaa 255
 Asp Val Val Ile Glu Arg Tyr His Ile Pro Arg Ala Cys Pro Arg Glu
 45 50 55
 gtg cag atg ggg gat ttt gtg cgc tac cac tac aac ggc act ttt gaa 303
 Val Gln Met Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Phe Glu
 60 65 70

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gat ggc aag aag ttt gat tca agc tat gat cgc aac acc ttg gtg gcc	351
Asp Gly Lys Lys Phe Asp Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala	
75 80 85 90	
atc gtg gtg ggt gtg ggg cgc ctc atc act ggc atg gac cga ggc ctc	399
Ile Val Val Gly Val Gly Arg Leu Ile Thr Gly Met Asp Arg Gly Leu	
95 100 105	
atg ggc atg tgt gtc aac gag cgg cga cgc ctc att gtg cct ccc cac	447
Met Gly Met Cys Val Asn Glu Arg Arg Arg Leu Ile Val Pro Pro His	
110 115 120	
ctg ggc tat ggg agc atc ggc ctg gcg ggg ctc att cca ccg gat gcc	495
Leu Gly Tyr Gly Ser Ile Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala	
125 130 135	
acc ctc tac ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac	543
Thr Leu Tyr Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp	
140 145 150	
acc gtg cag gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg	591
Thr Val Gln Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met	
155 160 165 170	
gtc cag gac ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg	639
Val Gln Asp Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu	
175 180 185	
gac ggc acc tcc ttc gac acc agc tac agt aag ggc ggc act tat gac	687
Asp Gly Thr Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp	
190 195 200	
acc tac gtc ggc tct ggt tgg ctg atc aag ggc atg gac cag ggg ctg	735
Thr Tyr Val Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu	
205 210 215	
ctg ggc atg tgt cct gga gag aga agg aag att atc atc cct cca ttc	783
Leu Gly Met Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe	
220 225 230	
ctg gcc tat ggc gag aaa ggc tat ggg acg gtg atc ccc cca cag gcc	831
Leu Ala Tyr Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala	
235 240 245 250	
tcg ctg gtc ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac	879
Ser Leu Val Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp	

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255	260	265	
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Ala Val Gln Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg			
270	275	280	
gcc ggg gcc ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg			975
Ala Gly Ala Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met			
285	290	295	
gac ggc acc ctc ttc gat tcc agc tac tcc cgc aac cac acc tac aat			1023
Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn			
300	305	310	
acc tat atc ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg			1071
Thr Tyr Ile Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu			
315	320	325	330
cag ggt gcc tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac			1119
Gln Gly Ala Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His			
335	340	345	
ctc gcc tat ggg gag aat gga act gga gac aag atc cct ggc tct gcc			1167
Leu Ala Tyr Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala			
350	355	360	
gtg cta atc ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat			1215
Val Leu Ile Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp			
365	370	375	
gtg gtg gaa atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag			1263
Val Val Glu Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu			
380	385	390	
acc acc aag ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg			1311
Thr Thr Lys Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu			
395	400	405	410
ctg gac ggc acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag			1359
Leu Asp Gly Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln			
415	420	425	
gag gcg act ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc			1407
Glu Ala Thr Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly			
430	435	440	
ctg cag ggc atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg			1455

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Leu Gln Gly Met Cys Val Gly Glu Arg Arg Gln Leu Ile Val Pro Pro
 445 450 455
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 His Leu Ala His Gly Glu Ser Gly Ala Arg Gly Val Pro Gly Ser Ala
 460 465 470
 gtg ctg ctg ttt gag gtg gag ctg gtg tcc cgg gag gat ggg ctg ccc 1551
 Val Leu Leu Phe Glu Val Glu Leu Val Ser Arg Glu Asp Gly Leu Pro
 475 480 485 490
 aca ggc tac ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt 1599
 Thr Gly Tyr Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe
 495 500 505
 gaa gac atg gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc 1647
 Glu Asp Met Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe
 510 515 520
 tcc acc ttc atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg 1695
 Ser Thr Phe Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met
 525 530 535
 cct ggg cag gac cct gag aaa acc ata gga gac atg ttc cag aac cag 1743
 Pro Gly Gln Asp Pro Glu Lys Thr Ile Gly Asp Met Phe Gln Asn Gln
 540 545 550
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 Asp Arg Asn Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys
 555 560 565 570
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 Ser Asp Glu Asp Glu Glu Arg Val His Glu Glu Leu
 575 580
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 tccctaagga accatagaag agaggaagaa aacaaagggc atgtgtgagg gaagctgctt 2500
 ggggtgggtgt tagggctatg aaatcttgga tttggggctg aggggtggga gggagggcag 2560
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Met Glu Leu Pro Ser Gly Pro Gly

1

5

ccg gag cgg ctc ttt gac tcg cac cgg ctt ccg ggt gac tgc ttc cta 160
 Pro Glu Arg Leu Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu

10

15

20

ctg ctc gtg ctg ctg ctc tac gcg cca gtc ggg ttc tgc ctc ctc gtc 208
 Leu Leu Val Leu Leu Leu Tyr Ala Pro Val Gly Phe Cys Leu Leu Val

25

30

35

40

ctg cgc ctc ttt ctc ggg atc cac gtc ttc ctg gtc agc tgc gcg ctg 256
 Leu Arg Leu Phe Leu Gly Ile His Val Phe Leu Val Ser Cys Ala Leu

45

50

55

cca gac agc gtc ctt cgc aga ttc gta gtg cgg acc atg tgt gcg gtg 304
 Pro Asp Ser Val Leu Arg Arg Phe Val Val Arg Thr Met Cys Ala Val

60

65

70

cta ggg ctc gtg gcc cgg cag gag gac tcc gga ctc cgg gat cac agt 352
 Leu Gly Leu Val Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Ser

75

80

85

gtc agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata 400
 Val Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile

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90	95	100	
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Val Asn Leu Leu Thr Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro			
105	110	115	120
agc ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg			496
Ser Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly			
125	130	135	
gag ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc			544
Glu Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro			
140	145	150	
ccc act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg			592
Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg			
155	160	165	
gag ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg			640
Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val			
170	175	180	
gta caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg			688
Val Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr			
185	190	195	200
gtg tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc			736
Val Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val			
205	210	215	
cct ttc acg gtg tat caa gta agg tgg ctt cgt cct gtt cat cgc caa			784
Pro Phe Thr Val Tyr Gln Val Arg Trp Leu Arg Pro Val His Arg Gln			
220	225	230	
cta ggg gaa gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg			832
Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val			
235	240	245	
gcc aag gaa ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa			880
Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys			
250	255	260	
gca gag cac atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca			928
Ala Glu His Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser			
265	270	275	280
gcc cag tct tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa			976

Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln	
285	290
295	
ctg gca act ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca	1024
Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro	
300	305
310	
ttg ggt gtc atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg	1072
Leu Gly Val Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu	
315	320
325	
act atc act aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac	1120
Thr Ile Thr Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp	
330	335
340	
atc acc aag gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt	1168
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410	
cagccctcac ccaactcaca acaggctgga tgggtgggtg gtaaaaaggg aaggatgagg	1430
ctcccccaat gtcacattaa attcatgggtt ttcattcaag gc	1472

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<210> 54
<211> 1652
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
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91/233

<222> (17)...(1468)

<400> 54

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aaagcggcgg cggagg atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc      52
      Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val
            1              5              10

ccg ggc ggg ccg gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc      100
Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser
      15              20              25

ggc ggc ggc cga gcc ctt cct caa ctc agc gat gac atc cct ttc cga      148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg
      30              35              40

gtc aac tgg ccc ggc acc gag ttc tct ctg ccc aca act gga gtt tta      196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu
      45              50              55              60

tat aaa gaa gat aat tat gtc atc atg aca act gca cat aaa gaa aaa      244
Tyr Lys Glu Asp Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys
            65              70              75

tat aaa tgc ata ctt ccc ctt gtg aca agt ggg gat gag gaa gaa gaa      292
Tyr Lys Cys Ile Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu
            80              85              90

aag gat tat aaa ggc cct aat cca aga gag ctt ttg gag cca cta ttt      340
Lys Asp Tyr Lys Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe
            95              100              105

aaa caa agc agt tgt tcc tac aga att gag tct tat tgg act tac gaa      388
Lys Gln Ser Ser Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu
            110              115              120

gta tgt cat gga aaa cac att cgg cag tac cat gaa gag aaa gaa act      436
Val Cys His Gly Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr
            125              130              135              140

ggt cag aaa ata aat att cac gag tac tac ctt ggg aat atg ttg gcc      484
Gly Gln Lys Ile Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala
            145              150              155

aag aac ctt cta ttt gaa aaa gaa cga gaa gca gaa gaa aag gaa aaa      532
Lys Asn Leu Leu Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys
            160              165              170

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92/233

tca aat gag att ccc act aaa aat atc gaa ggt cag atg aca cca tac	580
Ser Asn Glu Ile Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr	
175 180 185	
tat cct gtg gga atg gga aat ggt aca cct tgt agt ttg aaa cag aac	628
Tyr Pro Val Gly Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn	
190 195 200	
cgg ccc aga tca agt act gtg atg tac ata tgt cat cct gaa tct aag	676
Arg Pro Arg Ser Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys	
205 210 215 220	
cat gaa att ctt tca gta gct gaa gtt aca act tgt gaa tat gaa gtt	724
His Glu Ile Leu Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val	
225 230 235	
gtc att ttg aca cca ctc ttg tgc agt cat cct aaa tat agg ttc aga	772
Val Ile Leu Thr Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg	
240 245 250	
gca tct cct gtg aat gac ata ttt tgt caa tca ctg cca gga tct cca	820
Ala Ser Pro Val Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro	
255 260 265	
ttt aag ccc ctc acc ctg agg cag ctg gag cag cag gaa gaa ata cta	868
Phe Lys Pro Leu Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu	
270 275 280	
agg gtg cct ttt agg aga aat aaa gag gaa gat ttg caa tca act aaa	916
Arg Val Pro Phe Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys	
285 290 295 300	
gaa gag aga ttt cca gcg atc cac aag tcg att gct att ggc tct cag	964
Glu Glu Arg Phe Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln	
305 310 315	
cca gtg ctc act gtt ggg aca acc cac ata tcc aaa ttg aca gat gac	1012
Pro Val Leu Thr Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp	
320 325 330	
caa ctc ata aaa gag ttt ctt agt ggt tct tac tgc ttt cgt ggg ggt	1060
Gln Leu Ile Lys Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly	
335 340 345	
gtc ggt tgg tgg aaa tat gaa ttc tgc tat ggc aaa cat gta cat caa	1108
Val Gly Trp Trp Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln	

93/233

350	355	360	
tac cat gag gac aag gat agt ggg aaa acc tct gtg gtt gtc ggg aca			1156
Tyr His Glu Asp Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr			
365	370	375	380
tgg aac caa gaa gag cat att gaa tgg gct aag aag aat act gct aga			1204
Trp Asn Gln Glu Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg			
385	390	395	
gct tat cat ctt caa gac gat ggt acc cag aca gtc agg atg gtg tca			1252
Ala Tyr His Leu Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser			
400	405	410	
cat ttt tat gga aat gga gat att tgt gat ata act gac aaa cca aga			1300
His Phe Tyr Gly Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg			
415	420	425	
cag gtg act gta aaa cta aag tgc aaa gaa tca gat tca cct cat gct			1348
Gln Val Thr Val Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala			
430	435	440	
gtt act gta tat atg cta gag cct cac tcc tgt caa tat att ctt ggg			1396
Val Thr Val Tyr Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly			
445	450	455	460
gtt gaa tct cca gtg atc tgt aaa atc tta gat aca gca gat gaa aat			1444
Val Glu Ser Pro Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn			
465	470	475	
gga ctt ctt tct ctc ccc aac taaaggatat taaagttagg ggaaa			1490
Gly Leu Leu Ser Leu Pro Asn			
480			
gaaaagatca ttgaaagtca tgataatttc tgtccactg tgtctcatta tagagttctc			1550
agccattgga cctcttctaa aggatggtat aaaatgactc tcaaccactt tgtgaataca			1610
tatgtgtata taagaggta ttgataaact tctgaggcag ac			1652

<210> 55

<211> 2112

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

94/233

<222> (20)...(1843)

<400> 55

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atatttggtgg gtgagcagc atg ggc ttt gag gag ctg ctg gag cag gtg ggc      52
      Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly
              1              5              10

ggc ttt ggg ccc ttc caa ctg cgg aat gtg gca ctg ctg gcc ctg ccc      100
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro
              15              20              25

cga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc      148
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala
              30              35              40

gtg cct gcc cac cga tgt gcc ctg ccg ggt gcc cct gcc aac ttc agc      196
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser
              45              50              55

cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc      244
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly
              60              65              70              75

acg ctc agc tcc tgc ctc cgc ttt gcc tat ccc cag gct ctc ccc aac      292
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn
              80              85              90

acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa      340
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu
              95              100              105

cct gcc aca gtg ccc tgc tct cag ggc tgg gag tac gac cac tca gaa      388
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu
              110              115              120

ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc      436
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile
              125              130              135

cat ctg gag gtg gaa tgt cgg tgg agg cag tct ccc tgg gag gca gca      484
His Leu Glu Val Glu Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala
              140              145              150              155

ggt cga ggc ctt cct tgg gaa gaa gct gag gct gca gga ctg ggg agg      532
Gly Arg Gly Leu Pro Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg
              160              165              170

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95/233

gac aaa gtt tcc tat tcc cca agc tgg cgt gaa tcg ttg gga ggt tta	580
Asp Lys Val Ser Tyr Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu	
175 180 185	
tta tct ggc atg gag tgg gat ctg gtg tgt gag cag aaa ggt ctg aac	628
Leu Ser Gly Met Glu Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn	
190 195 200	
aga gct gcg tcc act ttc ttc ttc gcc ggt gtg ctg gtg ggg gct gtg	676
Arg Ala Ala Ser Thr Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val	
205 210 215	
gcc ttt gga tat ctg tcc gac agg ttt ggg cgg cgg cgt ctg ctg ctg	724
Ala Phe Gly Tyr Leu Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu	
220 225 230 235	
gta gcc tac gtg agt acc ctg gtg ctg ggc ctg gca tct gca gcc tcc	772
Val Ala Tyr Val Ser Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser	
240 245 250	
gtc agc tat gta atg ttt gcc atc acc cgc acc ctt act ggc tca gcc	820
Val Ser Tyr Val Met Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala	
255 260 265	
ctg gct ggt ttt acc atc atc gtg atg cca ctg gag ctg gag tgg ctg	868
Leu Ala Gly Phe Thr Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu	
270 275 280	
gat gtg gag cac cgc acc gtg gct gga gtc ctg agc agc acc ttc tgg	916
Asp Val Glu His Arg Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp	
285 290 295	
aca ggg ggc gtg atg ctg ctg gca ctg gtt ggg tac ctg ata cgg gac	964
Thr Gly Gly Val Met Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp	
300 305 310 315	
tgg cga tgg ctt ctg cta gct gtc acc ctg cct tgt gcc cca ggc atc	1012
Trp Arg Trp Leu Leu Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile	
320 325 330	
ctc agc ctc tgg tgg gtg cct gag tct gca cgc tgg ctt ctg acc caa	1060
Leu Ser Leu Trp Trp Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln	
335 340 345	
ggc cat gtg aaa gag gcc cac agg tac ttg ctc cac tgt gcc agg ctc	1108
Gly His Val Lys Glu Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu	

96/233

350	355	360	
aat ggg cgg cca gtg tgt gag gac agc ttc agc cag gag gct gtg agc			1156
Asn Gly Arg Pro Val Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser			
365	370	375	
aaa gtg gcc gcc ggg gaa cgg gtg gtc cga aga cct tca tac cta gac			1204
Lys Val Ala Ala Gly Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp			
380	385	390	395
ctg ttc cgc aca cca cgg ctc cga cac atc tca ctg tgc tgc gtg gtg			1252
Leu Phe Arg Thr Pro Arg Leu Arg His Ile Ser Leu Cys Cys Val Val			
400	405	410	
gtg tgg ttc gga gtg aac ttc tcc tat tac ggc ctg agt ctg gat gtg			1300
Val Trp Phe Gly Val Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val			
415	420	425	
tcg ggg ctg ggg ctg aac gtg tac cag aca cag ctg ttg ttc ggg gct			1348
Ser Gly Leu Gly Leu Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala			
430	435	440	
gtg gaa ctg ccc tcc aag ctg ctg gtc tac ttg tcg gtg cgc tac gca			1396
Val Glu Leu Pro Ser Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala			
445	450	455	
gga cgc cgc ctc acg caa gcc ggg aca ctg ctg ggc acg gcc ctg gcg			1444
Gly Arg Arg Leu Thr Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala			
460	465	470	475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act			1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr			
480	485	490	
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act			1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr			
495	500	505	
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctc aga cag aca			1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr			
510	515	520	
ggg atg ggg ctg act gca ctg gtg ggc cgg ctg ggg ggc tct ttg gcc			1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala			
525	530	535	
cca ctg gcg gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt			1684

97/233

Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
 540 545 550 555
 act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctc ctg ctg 1732
 Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
 560 565 570
 cca gag acg agg cag gca cag ctg cca gag acc atc cag gac gtg gag 1780
 Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
 575 580 585
 aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag 1828
 Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
 590 595 600
 cag gtc cag aac taagtgggag tggaggcagg cctccacag aagctctgca 1880
 Gln Val Gln Asn
 605
 gcaggggctg ggagagcaga agggcaggcc ctgcaactca ggctgggagt atcgaaccct 1940
 ctgcctaggg cgggagttgc tgccagtacc cgctccctct gctcatccat ccttgattat 2000
 ttggettcta ggaacagttg acttcccaga atgcagtggg ctgctgggca cccctctcac 2060
 ggttggggag gattctgtaa ataaaggtgc cccttggggtt ggggcagtgg tg 2112

<210> 56

<211> 1087

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (33)...(977)

<400> 56

agagggggcg tcaggccgcg ggagaggagg cc atg ggc gcg cgc ggg gcg ctg 53
 Met Gly Ala Arg Gly Ala Leu
 1 5
 ctg ctg gcg ctg ctg ctg gct cgg gct gga ctc agg aag ccg gag tcg 101
 Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
 10 15 20
 cag gag gcg gcg ccg tta tca gga cca tgc ggc cga cgg gtc atc acg 149
 Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr

98/233

25	30	35	
tgc cgc atc gtg ggt gga gag gac gcc gaa ctc ggg cgt tgg ccg tgg			197
Ser Arg Ile Val Gly Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp			
40	45	50	55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg			245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu			
60	65	70	
ctc agc cac cgc tgg gca ctc acg ggc ggc cac tgc ttt gaa acc tat			293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr			
75	80	85	
agt gac ctt agt gat ccc tcc ggg tgg atg gtc cag ttt ggc cag ctg			341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu			
90	95	100	
act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac			389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr			
105	110	115	
ttc gta tgc aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc			437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro			
120	125	130	135
tat gac att gcc ttg gtg aag ctg tct gca cct gtc acc tac act aaa			485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys			
140	145	150	
cac atc cag ccc atc tgt ctc cag gcc tcc aca ttt gag ttt gag aac			533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe Glu Asn			
155	160	165	
cgg aca gac tgc tgg gtg act ggc tgg ggg tac atc aaa gag gat gag			581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Glu Asp Glu			
170	175	180	
gca ctg cca tct ccc cac acc ctc cag gaa gtt cag gtc gcc atc ata			629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile			
185	190	195	
aac aac tct atg tgc aac cac ctc ttc ctc aag tac agt ttc cgc aag			677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys			
200	205	210	215
gac atc ttt gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag			725

99/233

Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn Ala Gln Gly Gly Lys
 220 225 230
 gat gcc tgc ttc ggt gac tca ggt gga ccc ttg gcc tgt aac aag aat 773
 Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu Ala Cys Asn Lys Asn
 235 240 245
 gga ctg tgg tat cag att gga gtc gtg agc tgg gga gtg ggc tgt ggt 821
 Gly Leu Trp Tyr Gln Ile Gly Val Val Ser Trp Gly Val Gly Cys Gly
 250 255 260
 cgg ccc aat cgg ccc ggt gtc tac acc aat atc agc cac cac ttt gag 869
 Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile Ser His His Phe Glu
 265 270 275
 tgg atc cag aag ctg atg gcc cag agt ggc atg tcc cag cca gac ccc 917
 Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met Ser Gln Pro Asp Pro
 280 285 290 295
 tcc tgg ccg cta ctc ttt ttc cct ctt ctc tgg gct ctc cca ctc ctg 965
 Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu
 300 305 310
 ggg ccg gtc tgagcctacc tgagcccatg cagcctgggg ccactgccaa gtcagg 1020
 Gly Pro Val

ccctggttct cttctgtctt gtttggtaat aaacacattc cagttgatgc cttgcagggc 1080
 attcttc 1087

<210> 57

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (216)...(500)

<400> 57

cccgaagttt gaggggtgtg gacggtttgt gacccctta gccgacccta ctctcactg 60
 gccgggacaa ctggtcttat cacggaggct ggggccagge agcccttcgg ttogggtggg 120
 cccatggacc ccagtccaac gccgagggaa taggaccatc caaaagcgga accttcgct 180
 cagaaaaagg cgtggaccct gccagcagcc aggcc atg gag ctc tct gat gtc 233

100/233

Met Glu Leu Ser Asp Val

1

5

acc ctc att gag ggt gtg ggt aat gag gtg atg gtg gtg gca ggt gtg 281

Thr Leu Ile Glu Gly Val Gly Asn Glu Val Met Val Val Ala Gly Val

10

15

20

gtg gtg ctg att cta gcc ttg gtc cta gct tgg ctc tct acc tac gta 329

Val Val Leu Ile Leu Ala Leu Val Leu Ala Trp Leu Ser Thr Tyr Val

25

30

35

gca gac agc ggt agc aac cag ctc ctg ggc gct att gtg tca gca ggc 377

Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly Ala Ile Val Ser Ala Gly

40

45

50

gac aca tcc gtc ctc cac ctg ggg cat gtg gac cac ctg gtg gca ggc 425

Asp Thr Ser Val Leu His Leu Gly His Val Asp His Leu Val Ala Gly

55

60

65

70

caa ggc aac ccc gag cca act gaa ctc ccc cat cca tca gag gca aat 473

Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro His Pro Ser Glu Ala Asn

75

80

85

act tcc ctg gac aag aaa gcc aga tgaaactgat ctaccagggc cgc 520

Thr Ser Leu Asp Lys Lys Ala Arg

90

ctgctacaag acccagcccg cacactgcgt tctctgaaca ttaccgacaa ctgtgtgatt 580

cactgccacc gctcaccccc agggtcagct gttccaggcc cctcagcctc cttggccccc 640

tcggccactg agccaccag ccttggtgtc aatgtgggca gcctcatggt gcctgtcttt 700

gtggtgctgt tgggtgtggt ctggtacttc cgaatcaatt accgccaatt cttcacagca 760

cctgccactg tctccctggt gggagtcacc gtcttcttca gcttcctagt atttgggatg 820

tatggacgat aaggacatag gaagaaaatg aaaggcatgg tctttctcct ttatggcctc 880

cccacttttc ctggccagag ctgggcccga gggcggggga gggaggggtg gaaaggatgt 940

gatggaaatc tctccatag gacacaggag gcaagtatgc ggctcccct tctcatccac 1000

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gccccagca cccagggctg cctgcaaggg cagctcagca tggccccagc acaactccgt 1240

agggagcctg gagtatcctt ccattttotca gccaaatact catcttttga gactgaaatc 1300

acactggcgg gaatgaagat tgtgccagcc ttctcttatg ggcacctagc cgccttcacc 1360

ttcttctct accccttagc aggaataggg tgtcctcct tctttcaaag cactttgctt 1420

101/233

gcattttatt ttattttttt aagagtcctt catagagctc agtcaggaag gggatggggc 1480
 accaagccaa gccccagca ttgggagcgg ccaggccaca gctgctgctc ccgtagtcct 1540
 caggctgtaa gcaagagaca gcaactggccc ttggccagcg tcctaccctg cccaactcca 1600
 aggactgggt atggattgct gggccctagg ctcttgcttc tggggctatt ggagggtcag 1660
 tgtctgtgac tgaataaagt tccattttgt ggtc 1694

<210> 58

<211> 1522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)...(668)

<400> 58

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 1 5 10
 ctg atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg 98
 Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
 15 20 25
 ggc tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc 146
 Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
 30 35 40 45
 cgg aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca 194
 Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
 50 55 60
 gcc gtg ctg tgc gct agt ttc atg tcc ttt gcc gtg aag cgg cgc tgg 242
 Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
 65 70 75
 ttc gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc 290
 Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
 80 85 90
 tac atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg 338
 Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
 95 100 105

102/233

tac tgc cgc aca gtt gcc atc atc ggc gga ctt tct tgt gtt ggc cag	386
Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln	
110 115 120 125	
cgg tgc tgg gga gct gta ccg ccg gaa acc tgc cag ccg ctc cct gca	434
Arg Cys Trp Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala	
130 135 140	
gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt ggc cta	482
Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu	
145 150 155	
ctc act gca gca cag caa gga gga ccg gct ggc gta tct gaa cca tct	530
Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser	
160 165 170	
ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat	578
Pro Arg Arg Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His	
175 180 185	
cct ggc cct ggc ctt tct gtc agg cta cta cgt gac cct cgc tgc cca	626
Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro	
190 195 200 205	
gat cct ggc tgt act gct gcc ccc tgt cat gct gct cat tcatg	670
Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His	
210 215	
gcaatgttgc ttactggcac aacacgcggc gtgttgagtt ctggaaccag atgaagctcc	730
ttggagagag tgtgggcac ttcggaactg ctgtcatctg gccactgatg gctgagtttt	790
atggcaagag gctgagatgg gcacagggag ccaactgaggg tcaccctgcc ttctccttg	850
ctggcccagc tgcgtgttat ttatgctttt tgggtctgttt gtttgatctt ttgctttttt	910
aaaattgttt tttgcagtta agaggcagct catttgtcca aatttctggg ctgagcgett	970
gggagggcag gagccctggc actaatgctg tacaggtttt tttcctgtta ggagagctga	1030
ggccagctgc ccaactgagtc tcctgtccct gagaagggag tatggcaggg ctgggatgcg	1090
gctactgaga gtgggagagt gggagacaga ggaaggaaga tggagattgg aagtgagcaa	1150
atgtgaaaaa ttctctcttg aacctggcag atgcagctag gctctgcagt gctgtttgga	1210
gactgtgaga gggagtgcgt gtgttgacac atgtggatca ggcccaggaa gggcacaggg	1270
gctgagcact acagaagtca catgggttct cagggtatgc caggggcaga aacagtaccg	1330
gctctctgtc actcaccttg agagtagagc agaccctgtt ctgctctggg ctgtgaaggg	1390
gtggagcagg cagtggccag ctttgccctt cctgctgtct ctgtttctag ctccatggtt	1450
ggcctggtgg ggggtggagt ccctcccaaa caccagacca cacagtctc caaaaataaa	1510

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cattttatat ag

1522

<210> 59

<211> 1591

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)...(1426)

<400> 59

gaaaacagtt ccacgttgct tgaaattgaa aatcaagata aaa atg ttc aca att 55

Met Phe Thr Ile

1

aag ctc ctt ctt ttt att gtt cct cta gtt att tcc tcc aga att gat 103

Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser Ser Arg Ile Asp

5

10

15

20

caa gac aat tca tca ttt gat tct cta tct cca gag cca aaa tca aga 151

Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu Pro Lys Ser Arg

25

30

35

ttt gct atg tta gac gat gta aaa att tta gcc aat ggc ctc ctt cag 199

Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn Gly Leu Leu Gln

40

45

50

ttg gga cat ggt ctt aaa gac ttt gtc cat aag acg aag ggc caa att 247

Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr Lys Gly Gln Ile

55

60

65

aat gac ata ttt caa aaa ctc aac ata ttt gat cag tct ttt tat gat 295

Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp

70

75

80

cta tcg ctg caa acc agt gaa atc aaa gaa gaa gaa aag gaa ctg aga 343

Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg

85

90

95

100

aga act aca tat aaa cta caa gtc aaa aat gaa gag gta aag aat atg 391

Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met

105

110

115

tca ctt gaa ctc aac tca aaa ctt gaa agc ctc cta gaa gaa aaa att 439

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Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile	
120 125 130	
cta ctt caa caa aaa gtg aaa tat tta gaa gag caa cta act aac tta	487
Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu	
135 140 145	
att caa aat caa cct gaa act cca gaa cac cca gaa gta act tca ctt	535
Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu	
150 155 160	
aaa act ttt gta gaa aaa caa gat aat agc atc aaa gac ctt ctc cag	583
Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln	
165 170 175 180	
acc gtg gaa gac caa tat aaa caa tta aac caa cag cat agt caa ata	631
Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln Ile	
185 190 195	
aaa gaa ata gaa aat cag ctc aga agg act agt att caa gaa ccc aca	679
Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu Pro Thr	
200 205 210	
gaa att tct cta tct tcc aag cca aga gca cca aga act act ccc ttt	727
Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr Thr Pro Phe	
215 220 225	
ctt cag ttg aat gaa ata aga aat gta aaa cat gat ggc att cct gct	775
Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala	
230 235 240	
gaa tgt acc acc att tat aac aga ggt gaa cat aca agt ggc atg tat	823
Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr Ser Gly Met Tyr	
245 250 255 260	
gcc atc aga ccc agc aac tct caa gtt ttt cat gtc tac tgt gat gtt	871
Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val Tyr Cys Asp Val	
265 270 275	
ata tca ggt agt cca tgg aca tta att caa cat cga ata gat gga tca	919
Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg Ile Asp Gly Ser	
280 285 290	
caa aac ttc aat gaa acg tgg gag aac tac aaa tat ggt ttt ggg agg	967
Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr Gly Phe Gly Arg	
295 300 305	

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ctt gat gga gaa ttt tgg ttg ggc cta gag aag ata tac tcc ata gtg 1015
 Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile Tyr Ser Ile Val
 310 315 320
 aag caa tct aat tat gtt tta cga att gag ctg gaa gac tgg aaa gac 1063
 Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp
 325 330 335 340
 aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc 1111
 Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr
 345 350 355
 aac tat acg cta cat cta gtt gcg att act ggc aat gtc ccc aat gca 1159
 Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala
 360 365 370
 atc ccg gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca 1207
 Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala
 375 380 385
 aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg 1255
 Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp
 390 395 400
 cat gat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca 1303
 His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
 405 410 415 420
 aga gca aaa tct aag cca gag agg aga aga gga tta tct tgg aag tct 1351
 Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys Ser
 425 430 435
 caa aat gga agg tta tac tct ata aaa tca acc aaa atg ttg atc cat 1399
 Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His
 440 445 450
 cca aca gat tca gaa agc ttt gaa tgaactgagg caaatttaaa aggcaat 1450
 Pro Thr Asp Ser Glu Ser Phe Glu
 455 460
 aatttaaacaa ttaacctcat tccaagttaa tgtggtetaa taatctggta ttaaatectt 1510
 aagagaaagc ttgagaaata gatttttttt tatcttaaag tcaactgteta ttaaagatta 1570
 aacatacaat cacataacct t 1591

<210> 60

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<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)...(784)

<400> 60

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aacagtctgt ggagacagtt gtgtccctgt ggetttggtg cgcctgtgtg cactttctcc      60
ctccacctgg agcatgggct aacaccggag gaaaggaaaa gacagagtca gacaggggagc      120
ctggggagggg gcc atg gtg cca atg cac tta ctg ggg aga ctg gag aag      169
      Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys
              1              5              10
cgg ctt ctc ctc ctg tgc tgc gcc tcc ttc cta ctg ggg ctg gct ttg      217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu
              15              20              25
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca      265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr
              30              35              40
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc egg ttt ctg gaa      313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu
              45              50              55              60
tgg ggg ctt egg tcc cag ctc caa tca atg cag act gag agc cca ggg      361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly
              65              70              75
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca gtc tat      409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr
              80              85              90
gaa gag gcc gtg gtg gga cta gaa tcc cag tgc cgc ccc caa gag ttg      457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu
              95              100              105
gac caa cca ccc ccc tac agc act gtt gtg ata ccc cca gca cct gag      505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu
              110              115              120
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa      553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu

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125	130	135	140	
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct				601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro				
	145	150	155	
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc				649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser				
	160	165	170	
act gct cct gat ctg cag agc ttg gcg gca gtc ccc aca tta gag cct				697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro				
	175	180	185	
ctg act cca ccc cct gcc tat gat gtc tgc ttt ggt cac cct gat gat				745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp				
	190	195	200	
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact				790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro				
205	210	215		
ctoccaagat ttctcttctc tccacaccag acctcggttca tttgactaac attttccage				850
gcctactatg tgcagaaac aagtgtttct gcctggacat cataaatggg gacttggacc				910
ctgaggagag tcaggccacg gtaagccctt cccagctgag atatgggtgg cataatttga				970
gtcttctggc aacatttggt gacctacccc atatccaata tttccagcgt tagattgagg				1030
atgaggtagg gaggtgatcc agagaaggcg gagaaggaag aagtaacctc tgagtggcgg				1090
ctattgcttc tgttccaggt gctgttcgag ctgttagaac ccttaggctt gacagctttg				1150
tgagttatta ttgaaaaatg aggattccaa gagtcagagg agtttgataa tgtgcacgag				1210
ggcacactgc tagtaaataa cattaataa actggaatg				1249

<210> 61

<211> 392

<212> PRT

<213> Homo sapiens

<400> 61

Met	Glu	Gly	Val	Ser	Ala	Leu	Leu	Ala	Arg	Cys	Pro	Thr	Ala	Gly	Leu
1					5				10					15	
Ala	Gly	Gly	Leu	Gly	Val	Thr	Ala	Cys	Ala	Ala	Ala	Gly	Val	Leu	Leu
			20						25					30	
Tyr	Arg	Ile	Ala	Arg	Arg	Met	Lys	Pro	Thr	His	Thr	Met	Val	Asn	Cys

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35	40	45
Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys		
50	55	60
Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly		
65	70	75
Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His		
85	90	95
Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln		
100	105	110
Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln		
115	120	125
Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly		
130	135	140
Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met		
145	150	155
Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys		
165	170	175
His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys		
180	185	190
Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val		
195	200	205
Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala		
210	215	220
Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe		
225	230	235
Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly		
245	250	255
Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg		
260	265	270
Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu		
275	280	285
Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly		
290	295	300
Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu		
305	310	315
		320

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Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335
 Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350
 Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365
 Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380
 Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 62

<211> 497

<212> PRT

<213> Homo sapiens

<400> 62

Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
 1 5 10 15
 Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
 20 25 30
 Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
 35 40 45
 Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
 50 55 60
 Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
 65 70 75 80
 Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
 85 90 95
 Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
 100 105 110
 Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Trp Lys Gly Ala Ala
 115 120 125
 Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
 130 135 140
 Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala

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145	150	155	160
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu			
165	170	175	
Leu Cys Gly Pro Val Gly Pro Arg Leu His Glu Leu Leu Asp Asp Asn			
180	185	190	
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu			
195	200	205	
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro			
210	215	220	
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met			
225	230	235	240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp			
245	250	255	
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu			
260	265	270	
Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile			
275	280	285	
Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg			
290	295	300	
Glu Leu Met Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr			
305	310	315	320
Ser Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala			
325	330	335	
Ser Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val			
340	345	350	
Gly Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg			
355	360	365	
Ser Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu			
370	375	380	
Val Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu			
385	390	395	400
Ala Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala			
405	410	415	
Thr Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu			
420	425	430	

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Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
 435 440 445

Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
 450 455 460

Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
 465 470 475 480

Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
 485 490 495

Tyr

<210> 63

<211> 417

<212> PRT

<213> Homo sapiens

<400> 63

Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
 1 5 10 15

Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
 20 25 30

Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
 35 40 45

Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
 50 55 60

Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu Leu Gly
 65 70 75 80

Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
 85 90 95

Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
 100 105 110

Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
 115 120 125

Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val
 130 135 140

Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val Val Ala
 145 150 155 160

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Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser Gln Asn
 165 170 175
 Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu Leu Thr
 180 185 190
 Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met Ala Val
 195 200 205
 Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys Gln Pro
 210 215 220
 Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys
 225 230 235 240
 Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys
 245 250 255
 Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln
 260 265 270
 Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr
 275 280 285
 Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu
 290 295 300
 Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu Gln Ile
 305 310 315 320
 Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr
 325 330 335
 Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala
 340 345 350
 Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile
 355 360 365
 Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu
 370 375 380
 Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr
 385 390 395 400
 Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Arg
 405 410 415
 Leu

<210> 64

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<211> 649

<212> PRT

<213> Homo sapiens

<400> 64

Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly Ser His Gln Pro Ala
 1 5 10 15
 Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu Asp His Ile Leu Pro
 20 25 30
 Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu Val Val Gly Ser Val
 35 40 45
 Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly Asp Phe Val Phe Asp
 50 55 60
 Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala Gly Val Val Gly Arg
 65 70 75 80
 Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu Ser Phe Leu Gly Tyr
 85 90 95
 Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly Ala His Ser Ser Thr
 100 105 110
 Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala Val Ala Met Leu Cys
 115 120 125
 Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn Ala Val Phe Asp Ile
 130 135 140
 Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile Val Gln Lys Val Leu
 145 150 155 160
 His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met Leu Arg Asn Gly Gly
 165 170 175
 Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly Gly Ala Gly Met Leu
 180 185 190
 Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro Pro Ala Phe Thr Glu
 195 200 205
 Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met Leu Val Arg Ala Val
 210 215 220
 Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp Leu Leu Leu Cys Pro
 225 230 235 240
 Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys Ile Pro Leu Ile Lys

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245	250	255
Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala Ala Leu Trp Phe Cys		
260	265	270
Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser Glu Asp Gly His Lys		
275	280	285
Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu Val Ile Pro Phe Leu		
290	295	300
Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe Val Val Ala Glu Arg		
305	310	315
Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val Leu Leu Thr Phe Gly		
325	330	335
Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys Lys Leu Ile Ala Ala		
340	345	350
Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu Arg Cys Val Leu Arg		
355	360	365
Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe Arg Ser Ala Leu Ser		
370	375	380
Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn Ile Gly Lys Asn Leu		
385	390	395
Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg Tyr Tyr Arg Glu Ala		
405	410	415
Val Arg Leu Asn Pro Lys Tyr Val His Ala Met Asn Asn Leu Gly Asn		
420	425	430
Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala Glu Glu Leu Leu Ser		
435	440	445
Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala Ala Trp Met Asn Leu		
450	455	460
Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu Ala Ala Glu Gln Ser		
465	470	475
Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr Pro Asp Cys Tyr Tyr		
485	490	495
Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg His Val Asp Ala Leu		
500	505	510
Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro Glu His Ser Leu Ala		
515	520	525

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Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr Gly Asn Leu Ala Gln
 530 535 540
 Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu Ile Pro Asn Asp His
 545 550 555 560
 Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly Lys Ser Gln Lys Tyr
 565 570 575
 Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile Lys Ala Asn Pro Asn
 580 585 590
 Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu Tyr His Arg Trp Gly
 595 600 605
 His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile Ser Leu Gln Leu Asp
 610 615 620
 Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly Leu Leu Arg Arg Lys
 625 630 635 640
 Leu Glu Leu Met Gln Lys Lys Ala Val
 645

<210> 65

<211> 93

<212> PRT

<213> Homo sapiens

<400> 65

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Pro Val Ala
 1 5 10 15
 Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 20 25 30
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 35 40 45
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 50 55 60
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 65 70 75 80
 Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 85 90

116/233

<210> 66

<211> 425

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
 1 5 10 15
 Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
 20 25 30
 Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
 35 40 45
 Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
 50 55 60
 Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
 65 70 75 80
 His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
 85 90 95
 Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
 100 105 110
 Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
 115 120 125
 Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
 130 135 140
 Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
 145 150 155 160
 Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
 165 170 175
 Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
 180 185 190
 Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu
 195 200 205
 Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
 210 215 220
 Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
 225 230 235 240

117/233

Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255
 Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
 260 265 270
 Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
 275 280 285
 Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
 290 295 300
 Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
 305 310 315 320
 Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
 325 330 335
 Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
 340 345 350
 Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
 355 360 365
 Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
 370 375 380
 Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
 385 390 395 400
 Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
 405 410 415
 Lys Asp Cys Ala Asp Pro Cys Asp Ser
 420 425

<210> 67

<211> 149

<212> PRT

<213> Homo sapiens

<400> 67

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 1 5 10 15
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
 20 25 30
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile

118/233

35	40	45
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp		
50	55	60
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn		
65	70	75
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met		
85	90	95
Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile		
100	105	110
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val		
115	120	125
Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro		
130	135	140
Gly Tyr Leu Met Gly		
145		

<210> 68

<211> 396

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu		
1	5	10
Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala		
20	25	30
Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln		
35	40	45
Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr		
50	55	60
Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu		
65	70	75
Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp		
85	90	95
Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu		
100	105	110

119/233

Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
 115 120 125
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg
 130 135 140
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
 145 150 155 160
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys
 165 170 175
 Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val
 180 185 190
 Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser
 195 200 205
 Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser
 210 215 220
 Arg Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro
 225 230 235 240
 Thr Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser
 245 250 255
 Asp Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp
 260 265 270
 Ile Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln
 275 280 285
 Lys Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr
 290 295 300
 His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser
 305 310 315 320
 Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met
 325 330 335
 Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro
 340 345 350
 Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu
 355 360 365
 Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu
 370 375 380
 Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

120/233

385

390

395

<210> 69

<211> 350

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu Ser Glu Glu
 1 5 10 15
 Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu Gln Asp Lys
 20 25 30
 Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
 35 40 45
 Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
 50 55 60
 Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Met Ala Val
 65 70 75 80
 Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg Glu Lys Leu
 85 90 95
 Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp Arg Tyr Asp
 100 105 110
 Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu Leu Ser Cys
 115 120 125
 Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro Gly Gln Pro
 130 135 140
 Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr Asp Pro Phe
 145 150 155 160
 Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly Pro Arg Glu
 165 170 175
 Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu Asn Lys Ser
 180 185 190
 Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser Ser Phe Gln
 195 200 205
 Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln Ala Cys Glu
 210 215 220

121/233

Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg Thr Trp Val
 225 230 235 240
 Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg Glu Ala Val
 245 250 255
 Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp Gln Arg Pro
 260 265 270
 Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe Glu Trp Lys
 275 280 285
 Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala Asn Pro Trp
 290 295 300
 Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu Phe Lys Ala
 305 310 315 320
 Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys Ile Arg Lys
 325 330 335
 Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile Ser
 340 345 350

<210> 70

<211> 153

<212> PRT

<213> Homo sapiens

<400> 70

Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe Ser Ala
 1 5 10 15
 Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln Val Pro
 20 25 30
 Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr His Arg
 35 40 45
 Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly Ala Leu
 50 55 60
 Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp Ala Pro
 65 70 75 80
 Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe Arg Pro
 85 90 95
 Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr Ser Gly

122/233

100	105	110
Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met Leu Glu		
115	120	125
Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu Thr Val		
130	135	140
Phe Pro Ser Pro Ser Pro Gly Cys Asp		
145	150	

<210> 71

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 71

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ggggtcacgg cgtgcgccgc ggccggcggtg ttgctctacc ggatcgcgcg gaggatgaag	120
ccaacgcaca cgatgggtcaa ctgctggttc tgcaaccagg atacgctggt gccctatggg	180
aaccgcaact gctgggactg tccccactgc gagcagtaca acggcttcca ggagaacggc	240
gactacaaca agccgateccc cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc	300
gcgcccagcc tgcgcgaccc ttgcgagccg cagcagtggg tgagcagcca agtcctgctg	360
tgcaagaggt gcaaccacca ccagaccacc aagatcaagc agctggccgc cttcgtctcc	420
cgcgaggagg gcaggtatga cgaggaggtc gaggtgtacc ggcatcacct ggagcagatg	480
tacaagctgt gccggccgtg ccaagcggct gtggagtact acatcaagca ccagaaccgc	540
cagctgcgcg ccctgttgct cagccaccag ttcaagcgcc gggaggccga ccagaccac	600
gcacagaact tctctccgc cgtgaagtcc ccggtccagg tcatcctgct ccgtgccctc	660
gccttcctgg cctgcgcctt cctactgacc accgcgctgt atggggccag cggacacttc	720
gccccaggca ccaactgtgc cctggccctg ccacctggtg gcaatggctc agccacacct	780
gacaatggca ccaccctgg ggccgagggc tggeggcagt tgetgggctt actccccgag	840
cacatggcgg agaagctgtg tgaggcctgg gcctttgggc agagccacca gacgggcgtc	900
gtggcactgg gctactcac ctgcctgctg gcaatgctgc tggctggccg catcaggctc	960
cggaggatcg atgccttctg cacctgcctg tgggccctgc tgetggggct gcacctggct	1020
gagcagcacc tgcaggccgc ctcgcctagc tggctagaca cgetcaagtt cagcaccaca	1080
tctttgtgct gcctggttgg cttcacggcg gctgtggcca caaggaaggc aacggggcca	1140
cggaggttcc ggccccgaag gtcagagaag cagcca	1176

<210> 72

123/233

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 72

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ttcctgctgg agccagagct gccaggtcg gcgtgcgt ctctctggag ctgcgtgtgt      120
ctggggcccg cgcctgcgcc cccgggaccc gtctcccccg agggccggtt ggcggcagcc      180
tgggacgcgc ttatcgtgcg gccagtcgg cgtggcgcc gcgtggcagt gggagtcaat      240
gcatgtgttg atgtggtgct ctcaagggtg aagctcttgc aggcacttgg ccttagtctt      300
gggaatggga aagatcacag cattctgcat tcaaggaatg atctggaaga agccttcatt      360
cacttcatgt ggaaggaggc agctgctgag cgcttcttca gtgataagga aacttttcac      420
gacattgccc aggttgcgtc agagttccca ggagcccagc actatgtagg aggaaatgca      480
gctttaattg gacagaaatt tgcagccaac tcagatttaa aggttcttct ttgcgggtcca      540
gttggcccaa ggctacatga gcttcttgat gacaatgtct ttgttccacc agagtcattg      600
caggaagtgg atgagttcca cctcatttta gagtatcaag caggggagga gtggggccag      660
ttaaagctc cccatgccaa ccgattcctc ttctctcacg acctctocaa cggggccatg      720
aatatgctgg aggtgtttgt gtctagcctg gaggagtttc agccagacct ggtggtctc      780
tctggattgc acatgatgga gggacaaagc aaggagctcc agaggaagag actcttggag      840
gttgtaacct ccatttctga catccccact ggtattccag ttcacctaga gctggccagt      900
atgactaaca gggagctcat gaggcagcatt gtccatcagc aggtctttcc cgcggtgact      960
tcccttgggc tgaatgaaca ggagctgtta tttctcacc agtcagctc tggacctcac      1020
tcttctctct cttcctggaa cggtgttct gatgtgggca tggtcagtga catcctctc      1080
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gcagccgtgg ctgcaggagc tcgtgtggct gggacacagg cctgcgccac agaaccata      1260
gacaccagcc gagtgtctct gagggcacc caagagttca tgacttccca ttcggaggca      1320
ggctccagga ttgtattaaa cccaaacaag ccagtagtag aatggcacag agagggaata      1380
tcttccact tcacaccagt attggtgtgt aaagacccca ttcgaactgt aggccttggga      1440
gatgccattt cagccgaagg actcttctat tcggaagta caccctcacta t      1491
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<210> 73

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 73

124/233

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cgccectcc	gcttccagac	attctcagct	gtcaggtaact	ctgatggcta	cgcagctcc	120
tccctcctcc	gggccgtggc	ccacctgcgg	tcccagctct	gggcccacct	ccctcgagcc	180
cccctagctc	ccagatggag	cccctctgcc	tggtgctggg	ttgggggagc	cctgctaggc	240
cccatggtac	tgagtaagca	tccccacctc	tgccttgtgg	ccctgtgtga	ggcagaagag	300
gccccctcctg	ccagctccac	accccatgtc	gtgggggtctc	gctttaactg	gaagctcttc	360
tggcagtttc	tgcaccccca	cctgctggtc	ctgggggtag	ccgtcgtgct	ggccttgggt	420
gcggcactcg	tgaatgtaca	gatccccctg	ctcctgggcc	agctggtaga	ggtcgtggcc	480
aagtacacaa	gggaccacgt	agggagtttc	atgactgagt	cccagaatct	cagcaccac	540
ctgcttatcc	tctatggtgt	ccagggactg	ctgaccttcg	ggtacctggt	gctgctgtcc	600
cacgttggcg	agcgcattggc	tgtggacatg	cggagggccc	tcttcagctc	cctgctccgg	660
tactgccagc	cgcaggggtgc	agagttggga	caagacatca	ccttctttga	cgccaataag	720
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cttgtcatct	cccaggggct	gcgaagctgc	acccaggtgg	caggctgcct	ggtgtccctg	840
tccatgctgt	cgacacgcct	cacgctgctg	ctgatggtgg	ccacaccagc	cctgatggga	900
gtgggcaccc	tgatgggctc	aggcctccga	aaattgtctt	gccagtgtca	ggagcagatc	960
gccagggcaa	tgggcgtagc	agacgaggcc	ctgggcaatg	tgcggactgt	gcgtgccttc	1020
gccatggagc	aacgggaaga	ggagcgctat	ggggcagagc	tggaagcctg	ccgctgccgg	1080
gcagaggagc	tgggccgcgg	catgccttg	ttccaagggc	ttccaacat	cgccttcaac	1140
tgcattggtct	tgggtaccct	atattattggg	ggctcccttg	tggccggaca	gcagctgaca	1200
gggggagacc	tcatgtcctt	cctggtggcc	tccagacag	tgcaaaggct	g	1251

<210> 74

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 74

atgattccta	accagcataa	tgctggagcc	gggagccacc	aacctgcagt	tttcagaatg	60
gccgtgttgg	acactgattt	ggatcacatt	cttccatctt	ctgtttcttc	tccattctgg	120
gctaagttag	tagtgggatc	ggttgccatt	gtgtgttttg	cacgcagcta	tgatggagac	180
tttgtctttg	atgactcaga	agctattgtt	aacaataagg	ttgctggtgt	tgtcggccgt	240
gcagacctcc	tgtgtgccct	gttctttctg	ttatctttcc	ttggctactg	taaagcattt	300
agagaaagta	acaaggaggg	agcgcattct	tccaccttct	gggtgctgct	gagtatcttt	360
ctgggagcag	tggccatgct	gtgcaaagag	caagggatca	ctgtgctggg	tttaaatgcg	420
gtatttgaca	tcttgggtgat	aggcaaattc	aatgttctgg	aaattgtcca	gaagggtacta	480

125/233

cataaggaca agtcattaga gaatctcgge atgtcagga acgggggcct cctcttcaga 540
atgaccctgc tcacctctgg aggggctggg atgtctctacg tgcgctggag gatcatgggc 600
acggggccgc cggccttcac cgaggctggac aaccggcct cctttgctga cageatgctg 660
gtgagggcg taaactacaa ttactactat tcattgaatg cctggctgct gctgtgtccc 720
tgggtgctgt gttttgattg gtcaatgggc tgcaccccc tcattaagtc catcagcgac 780
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atcccatctt tccccgcgag taacctgttc ttccgagtgg gcttcgtggt cggcgagcgt 960
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gctgataaag gcaaccagac agctgccacc agatactacc ggggaagctgt aagattaaat 1260
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gctgtgcttt atcatcgttg gggacatcta gacttgcca agaaacacta tgaaatctcc 1860
ttgcagcttg accccacggc atcaggaact aaggagaatt acggtctgct gagaagaaag 1920
ctagaactaa tgcaaaagaa agctgtc 1947

<210> 75

<211> 279

<212> DNA

<213> Homo sapiens

<400> 75

atgateccac tgggtcacat cctcttctctg cttttgctcc cagtggctgc agctcagacg 60
actccaggag agagatcacc actccctgcc ttttaccctg gcaactcagg ctcttgttcc 120
ggatgtgggt cctctctctt gccgctcctg gcaggcctcg tggctgctga tgcggtggca 180
tcgctgctca tcgtgggggc ggtgttctctg tgcgcacgcc cagcgcgag ccccgcccaa 240

126/233

gaagatggca aagtctacat caacatgccca ggcaggggc

279

<210> 76

<211> 1275

<212> DNA

<213> Homo sapiens

<400> 76

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cttcagagg	gttggagcct	cccctcttac	gtctctgtgc	ttgtggctct	ggggaacctg	120
ggtctgctgg	tggtagccct	ctggaggagg	ctggccccag	gaaaggacga	gcagggtcccc	180
atccgggtgg	tgcagggtgt	gggcatgggt	ggcacagccc	tgtctggcctc	tctgtggcac	240
catgtggccc	cagtggcagg	acagttgcat	tctgtggcct	tcttagcaact	ggcctttgtg	300
ctggcactgg	catgctgtgc	ctcgaatgtc	actttctgtc	ccttcttgag	ccacctgccca	360
cctcgcttct	tacgggtcatt	cttcctgggt	caaggcctga	gtgccctgct	gccctgctgt	420
ctggccctag	tgcagggtgt	gggcgcctc	gagtgccgc	cagcccccat	caacggcacc	480
cctggccccc	cgtctgaact	ccttgagcgt	tttcccgccca	gcaccttctt	ctgggcactg	540
actgcccttc	tggctgcttc	agctgctgcc	ttccagggtc	ttctgctgct	gttgccgccca	600
ccaccatctg	taccacacagg	ggagtttaga	tcaggcctcc	aggtgggagc	cccaggagca	660
gaggaagagg	tggaagagtc	ctcaccactg	caagagccac	caagccaggc	agcaggcacc	720
acccctggtc	cagaccctaa	ggcctatcag	cttctatcag	cccgcagtgc	ctgcctgctg	780
ggcctgttgg	ccgccaccaa	cgcgtgacc	aatggcgtgc	tgctgcccgt	gcagagcttt	840
tcctgcttac	cctacgggcg	tctggcctac	cacctggctg	tgggtgctggg	cagtgtgtcc	900
aatcccctgg	cctgcttcct	ggccatgggt	gtgctgtgca	ggtccttggc	agggctgggc	960
ggcctctctc	tgtctggcgt	gttctgtggg	ggctacctga	tggcgtggc	agtctgagc	1020
ccctgcccgc	ccctggtggg	cacctcggcg	ggggtgggtcc	tcgtggtgct	gtcgtgggtg	1080
ctgtgtcttg	gcgtgttctc	ctacgtgaag	gtggcagcca	gctccctgct	gcattggcggg	1140
ggccggccgg	cattgctggc	agccggcgtg	gcatccagg	tgggctctct	gtcgggcgtc	1200
gttgctatgt	tccccccgac	cagcatctat	cacgtgttcc	acagcagaaa	ggactgtgca	1260
gaccctgtg	actcc					1275

<210> 77

<211> 447

<212> DNA

<213> Homo sapiens

<400> 77

127/233

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ttcataatcc tggaccgac gaatgcacca aatatcccaa aactcaatag attccttctt	360
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<210> 78

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 78

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atctattact tagcgatctt tcagtgtaat tggcctgaag tgaaaaccac agcctctgat	180
ggtgaacaga ccacacgtga gcctgtgctc aaagccatgt ttttggctga caccatttg	240
cttggggaat tcctaggcca ctggctggac aaattacgaa gggaatggca gatggagaga	300
gogttccaga cagctctgtg gttgctgcag ccggaagtgc tcttcacccg gggggatata	360
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ggcttccatt atgagatgaa cacatacaaa gtagaacgct ttgagaaagt gttcagctct	540
gaaagactgt tttcttggaa aggcattaac tttgtgatgg tcaacagcgt ggcgctgaac	600
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ctgaactgct cccgagaggc acgtggctcc agccgggtgtg gacctgggccc tctgctgccc	720
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cccacagact acacctctc caagtgtac ctcccacgtg aggatgtggt tttgatcacc	1080
tactgtggag tgggtgggctt ccttgtggtc ctccactca ctacttttg gcttctagcc	1140
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128/233

<210> 79

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 79

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gccgtcttcc	tgggtctaccg	gaccatcaca	gactttcgtg	agaaactcaa	gcaccctgtc	300
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aagatgtcac	tggtaaagac	caaggaggag	gatgggcggg	aagcagtggg	gttccggcag	780
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gccaatcctt	ggaacacaat	tgtcttcttc	tgtgggcct	tcttggcatt	atttaaagca	960
gcagagtttg	ccaaactgag	tataaaatgg	atgatcaaaa	ttagaaagag	ataccttaaa	1020
agaagaggtc	aggcaacgag	ccacataagc				1050

<210> 80

<211> 459

<212> DNA

<213> Homo sapiens

<400> 80

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ctgggcgtat	gccggacca	ccgcctggcg	gagatcatat	actggattcg	ctgtctccac	180
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ccggtggcgc	gaggcggaag	cccggctcgg	ttcccaggat	tccggcctgc	agcgaggggg	300
ctagcgcagt	gccagctcg	ctgggtgacc	tggggcacgg	ctcgtccct	cctcggcttc	360

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agtttgcta totgtatgtt ggagcttcta ctccacattt cttctcccct aactccagcc 420
cctgaaaccg tottccccag tccctccccg ggctgcgac 459

<210> 81

<211> 4027

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)...(1370)

<400> 81

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gcccgcctac ccgcctacc gcctaccgc ctacccccct gccggcctgc cgtcctcca 180
cgcgagagc c atg gag gga gtg agc gcg ctg ctg gcc cgc tgc ccc acg 230
Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr
1 5 10
gcc ggc ctg gcc ggc ggc ctg ggg gtc acg gcg tgc gcc gcg gcc ggc 278
Ala Gly Leu Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly
15 20 25
gtg ttg ctc tac cgg atc gcg cgg agg atg aag cca acg cac acg atg 326
Val Leu Leu Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met
30 35 40 45
gtc aac tgc tgg ttc tgc aac cag gat acg ctg gtg ccc tat ggg aac 374
Val Asn Cys Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn
50 55 60
cgc aac tgc tgg gac tgt ccc cac tgc gag cag tac aac ggc ttc cag 422
Arg Asn Cys Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln
65 70 75
gag aac ggc gac tac aac aag ccg atc ccc gcc cag tac ttg gag cac 470
Glu Asn Gly Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His
80 85 90
ctg aac cac gtg gtg agc agc gcg ccc agc ctg cgc gac cct tcg cag 518
Leu Asn His Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln
95 100 105

130/233

ccg cag cag tgg gtg agc agc caa gtc ctg ctg tgc aag agg tgc aac	566
Pro Gln Gln Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn	
110 115 120 125	
cac cac cag acc acc aag atc aag cag ctg gcc gcc ttc gct ccc cgc	614
His His Gln Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg	
130 135 140	
gag gag ggc agg tat gac gag gag gtc gag gtg tac cgg cat cac ctg	662
Glu Glu Gly Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu	
145 150 155	
gag cag atg tac aag ctg tgc cgg ccg tgc caa gcg gct gtg gag tac	710
Glu Gln Met Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr	
160 165 170	
tac atc aag cac cag aac cgc cag ctg cgc gcc ctg ttg ctc agc cac	758
Tyr Ile Lys His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His	
175 180 185	
cag ttc aag cgc cgg gag gcc gac cag acc cac gca cag aac ttc tcc	806
Gln Phe Lys Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser	
190 195 200 205	
tcc gcc gtg aag tcc ccg gtc cag gtc atc ctg ctc cgt gcc ctc gcc	854
Ser Ala Val Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala	
210 215 220	
ttc ctg gcc tgc gcc ttc cta ctg acc acc gcg ctg tat ggg gcc agc	902
Phe Leu Ala Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser	
225 230 235	
gga cac ttc gcc cca ggc acc act gtg ccc ctg gcc ctg cca cct ggt	950
Gly His Phe Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly	
240 245 250	
ggc aat ggc tca gcc aca cct gac aat ggc acc acc cct ggg gcc gag	998
Gly Asn Gly Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu	
255 260 265	
ggc tgg cgg cag ttg ctg ggc cta ctc ccc gag cac atg gcg gag aag	1046
Gly Trp Arg Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys	
270 275 280 285	
ctg tgt gag gcc tgg gcc ttt ggg cag agc cac cag acg ggc gtc gtg	1094
Leu Cys Glu Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val	

131/233

290	295	300	
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Ala Leu Gly Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg			
305	310	315	
atc agg ctc cgg agg atc gat gcc ttc tgc acc tgc ctg tgg gcc ctg			1190
Ile Arg Leu Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu			
320	325	330	
ctg ctg ggg ctg cac ctg gct gag cag cac ctg cag gcc gcc tgc cct			1238
Leu Leu Gly Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro			
335	340	345	
agc tgg cta gac acg ctc aag ttc agc acc aca tct ttg tgc tgc ctg			1286
Ser Trp Leu Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu			
350	355	360	365
gtt ggc ttc acg gcg gct gtg gcc aca agg aag gca acg ggc cca cgg			1334
Val Gly Phe Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg			
370	375	380	
agg ttc cgg ccc cga agg tca gag aag cag cca tgactgcggg ggg			1380
Arg Phe Arg Pro Arg Arg Ser Glu Lys Gln Pro			
385	390		
aggacacacg gatgctcagg cccaggcttt gccagggtccg aagcgggccc ctctctgtcc			1440
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tgctttt 4027

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<210> 82

<211> 2495

<212> DNA

<213> Homo sapiens

<220>

133/233

<221> CDS

<222> (30)...(1523)

<400> 82

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                               1             5

tac gcg ggc ttc ctg gcg ctg gcc gtg ggc tgc gtc ttc ctg ctg gag      101
Tyr Ala Gly Phe Leu Ala Leu Ala Val Gly Cys Val Phe Leu Leu Glu
    10             15             20

cca gag ctg cca ggc tcg gcg ctg cgc tct ctc tgg agc tcg ctg tgt      149
Pro Glu Leu Pro Gly Ser Ala Leu Arg Ser Leu Trp Ser Ser Leu Cys
    25             30             35             40

ctg ggg ccc gcg cct gcg ccc ccg gga ccc gtc tcc ccc gag ggc cgg      197
Leu Gly Pro Ala Pro Ala Pro Pro Gly Pro Val Ser Pro Glu Gly Arg
           45             50             55

ttg gcg gca gcc tgg gac gcg ctt atc gtg cgg cca gtc cgg cgc tgg      245
Leu Ala Ala Ala Trp Asp Ala Leu Ile Val Arg Pro Val Arg Arg Trp
           60             65             70

cgc cgc gtg gca gtg gga gtc aat gca tgt gtt gat gtg gtg ctc tca      293
Arg Arg Val Ala Val Gly Val Asn Ala Cys Val Asp Val Val Leu Ser
           75             80             85

ggg gtg aag ctc ttg cag gca ctt ggc ctt agt cct ggg aat ggg aaa      341
Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser Pro Gly Asn Gly Lys
           90             95             100

gat cac agc att ctg cat tca agg aat gat ctg gaa gaa gcc ttc att      389
Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu Ala Phe Ile
    105             110             115             120

cac ttc atg tgg aag gga gca gct gct gag cgc ttc ttc agt gat aag      437
His Phe Met Trp Lys Gly Ala Ala Ala Glu Arg Phe Phe Ser Asp Lys
           125             130             135

gaa act ttt cac gac att gcc cag gtt gcg tca gag ttc cca gga gcc      485
Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser Glu Phe Pro Gly Ala
           140             145             150

cag cac tat gta gga gga aat gca gct tta att gga cag aaa ttt gca      533
Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile Gly Gln Lys Phe Ala

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155	160	165	
gcc aac tca gat tta aag gtt ctt ctt tgc ggt cca gtt ggc cca agg			581
Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly Pro Val Gly Pro Arg			
170	175	180	
cta cat gag ctt ctt gat gac aat gtc ttt gtt cca cca gag tca ttg			629
Leu His Glu Leu Leu Asp Asp Asn Val Phe Val Pro Pro Glu Ser Leu			
185	190	195	200
cag gaa gtg gat gag ttc cac ctc att tta gag tat caa gca ggg gag			677
Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu Tyr Gln Ala Gly Glu			
205	210	215	
gag tgg ggc cag tta aaa gct ccc cat gcc aac cga ttc atc ttc tct			725
Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn Arg Phe Ile Phe Ser			
220	225	230	
cac gac ctc tcc aac ggg gcc atg aat atg ctg gag gtg ttt gtg tct			773
His Asp Leu Ser Asn Gly Ala Met Asn Met Leu Glu Val Phe Val Ser			
235	240	245	
agc ctg gag gag ttt cag cca gac ctg gtg gtc ctc tct gga ttg cac			821
Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val Leu Ser Gly Leu His			
250	255	260	
atg atg gag gga caa agc aag gag ctc cag agg aag aga ctc ttg gag			869
Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg Lys Arg Leu Leu Glu			
265	270	275	280
gtt gta acc tcc att tct gac atc ccc act ggt att cca gtt cac cta			917
Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly Ile Pro Val His Leu			
285	290	295	
gag ctg gcc agt atg act aac agg gag ctc atg agc agc att gtc cat			965
Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met Ser Ser Ile Val His			
300	305	310	
cag cag gtc ttt ccc gcg gtg act tcc ctt ggg ctg aat gaa cag gag			1013
Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly Leu Asn Glu Gln Glu			
315	320	325	
ctg tta ttt ctc acc cag tca gcc tct gga cct cac tct tct ctc tct			1061
Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro His Ser Ser Leu Ser			
330	335	340	
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Ser Trp Asn Gly Val Pro Asp Val Gly Met Val Ser Asp Ile Leu Phe
 345 350 355 360
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 Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser Arg Ala Ser Asp Leu
 365 370 375
 acc agg atc cat ttc cac acg ctg gtc tac cac atc ctg gca act gtg 1205
 Thr Arg Ile His Phe His Thr Leu Val Tyr His Ile Leu Ala Thr Val
 380 385 390
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 Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val Ala Ala Gly Ala Arg
 395 400 405
 gtg gct ggg aca cag gcc tgc gcc aca gaa acc ata gac acc agc cga 1301
 Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr Ile Asp Thr Ser Arg
 410 415 420
 gtg tct ctg agg gca ccc caa gag ttc atg act tcc cat tcg gag gca 1349
 Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr Ser His Ser Glu Ala
 425 430 435 440
 ggc tcc agg att gta tta aac cca aac aag cca gta gta gaa tgg cac 1397
 Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro Val Val Glu Trp His
 445 450 455
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 Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val Leu Val Cys Lys Asp
 460 465 470
 ccc att cga act gta ggc ctt gga gat gcc att tca gcc gaa gga ctc 1493
 Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile Ser Ala Glu Gly Leu
 475 480 485
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 Phe Tyr Ser Glu Val His Pro His Tyr
 490 495
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<210> 83

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1320)

<400> 83

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gtcagc atg ctg gtg cat tta ttt cgg gtc ggg att cgg ggt ggc cca 108
Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
1 5 10
ttc cca ggc agg ctg cta ccg ccc ctc cgc ttc cag aca ttc tca gct 156
Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
15 20 25 30
gtc agg tac tct gat ggc tac cgc agc tcc tcc ctc ctc cgg gcc gtg 204
Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val
35 40 45
gcc cac ctg cgg tcc cag ctc tgg gcc cac ctc cct cga gcc ccc cta 252
Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
50 55 60
gct ccc aga tgg agc ccc tct gcc tgg tgc tgg gtt ggg gga gcc ctg 300
Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
65 70 75

137/233

cta ggc ccc atg gta ctg agt aag cat ccc cac ctc tgc ctt gtg gcc	348
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala	
80 85 90	
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc	396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val	
95 100 105 110	
gtg ggg tct cgc ttt aac tgg aag ctc ttc tgg cag ttt ctg cac ccc	444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro	
115 120 125	
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcg gca	492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala	
130 135 140	
ctc gtg aat gta cag atc ccc ctg ctc ctg ggc cag ctg gta gag gtc	540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val	
145 150 155	
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc	588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser	
160 165 170	
cag aat ctc agc acc cac ctg ctt atc ctc tat ggt gtc cag gga ctg	636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu	
175 180 185 190	
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg	684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met	
195 200 205	
gct gtg gac atg cgg agg gcc ctc ttc agc tcc ctg ctc cgg tac tgc	732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys	
210 215 220	
cag ccg cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc	780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala	
225 230 235	
aat aag aca ggg cag ctg gtg agc cgc ttg aca act gac gtg cag gag	828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu	
240 245 250	
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc	876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys	

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255	260	265	270	
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tog aca cgc				924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg				
275	280	285		
ctc acg ctg ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg ggc				972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly				
290	295	300		
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tgt cag gag				1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu				
305	310	315		
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg				1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val				
320	325	330		
cgg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat				1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr				
335	340	345	350	
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc				1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg				
355	360	365		
ggc atc gcc ttg ttc caa ggg ctt tcc aac atc gcc ttc aac tgc atg				1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met				
370	375	380		
gtc ttg ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag				1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln				
385	390	395		
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg				1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val				
400	405	410		
caa agg ctg tgacattcca tgcattggaag gaccatcctt gacaggctgt gtg				1360
Gln Arg Leu				
415				
agctgccctt ccccatgcct gccacttcca gggatgacaa gctgaccctt gtccccacac				1420
accccaccct tatagcttat tgctttgcgt tgggtccaaaa ccaccgcctc agctgagcct				1480
ctgggatgac cagagctgat caccagacag ctcaaggcgg gcctcccccc tectatctct				1540
ttccaagcta aacacaagca gttctacata aatatgttat ggtaaataat gagatagtaa				1600

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atatgctgta acagatc

1617

<210> 84

<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (260)...(2209)

<400> 84

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tagattcgag aagtgttta tcctttgact ggaaaagaaa agtagctgca gtattccccc      120
agcacttgct gagagcatgc cgtatgccag gctgtgaggg tcgagagaca agcagtggaa      180
gagttgcggc ctgtttcatc tctggattgt aaatctgagc ctccttctgg cccctggaag      240
gggacagcat cacgatgga atg att cct aac cag cat aat gct gga gcc ggg      292
          Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly
                1             5             10

agc cac caa cct gca gtt ttc aga atg gcc gtg ttg gac act gat ttg      340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu
          15             20             25

gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta      388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu
          30             35             40

gta gtg gga tcg gtt gcc att gtg tgt ttt gca cgc agc tat gat gga      436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly
          45             50             55

gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct      484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala
          60             65             70             75

ggg gtt gtc ggc cgt gca gac ctc ctg tgt gcc ctg ttc ttc ttg tta      532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu
          80             85             90

tct ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga      580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly
          95             100             105

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gcg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca	628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala	
110 115 120	
gtg gcc atg ctg tgc aaa gag caa ggg atc act gtg ctg ggt tta aat	676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn	
125 130 135	
gcg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att	724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile	
140 145 150 155	
gtc cag aag gta cta cat aag gac aag tca tta gag aat ctc ggc atg	772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met	
160 165 170	
ctc agg aac ggg ggc ctc ctc ttc aga atg acc ctg ctc acc tct gga	820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly	
175 180 185	
ggg gct ggg atg ctc tac gtg cgc tgg agg atc atg ggc acg ggc ccg	868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro	
190 195 200	
ccg gcc ttc acc gag gtg gac aac ccg gcc tcc ttt gct gac agc atg	916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met	
205 210 215	
ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg	964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp	
220 225 230 235	
ctg ctg ctg tgt ccc tgg tgg ctg tgt ttt gat tgg tca atg ggc tgc	1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys	
240 245 250	
atc ccc ctc att aag tcc atc agc gac tgg agg gta att gca ctt gca	1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala	
255 260 265	
gca ctc tgg ttc tgc cta att ggc ctg ata tgc caa gcc ctg tgc tct	1108
Ala Leu Trp Phe Cys Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser	
270 275 280	
gaa gac ggc cac aag aga agg atc ctt act ctg ggc ctg gga ttt ctc	1156
Glu Asp Gly His Lys Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu	

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285	290	295	
gtt atc cca ttt ctc ccc gcg agt aac ctg ttc ttc cga gtg ggc ttc			1204
Val Ile Pro Phe Leu Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe			
300	305	310	315
gtg gtc gcg gag cgt gtc ctc tac ctc ccc agc att ggg tac tgt gtg			1252
Val Val Ala Glu Arg Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val			
320	325	330	
ctg ctg act ttt gga ttc gga gcc ctg agc aaa cat acc aag aaa aag			1300
Leu Leu Thr Phe Gly Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys			
335	340	345	
aaa ctc att gcc gct gtc gtg ctg gga atc tta ttc atc aac acg ctg			1348
Lys Leu Ile Ala Ala Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu			
350	355	360	
aga tgt gtg ctg cgc agc ggc gag tgg cgg agt gag gaa cag ctt ttc			1396
Arg Cys Val Leu Arg Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe			
365	370	375	
aga agt gct ctg tct gtg tgt ccc ctc aat gct aag gtt cac tac aac			1444
Arg Ser Ala Leu Ser Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn			
380	385	390	395
att ggc aaa aac ctg gct gat aaa ggc aac cag aca gct gcc atc aga			1492
Ile Gly Lys Asn Leu Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg			
400	405	410	
tac tac cgg gaa gct gta aga tta aat ccc aag tat gtt cat gcc atg			1540
Tyr Tyr Arg Glu Ala Val Arg Leu Asn Pro Lys Tyr Val His Ala Met			
415	420	425	
aat aat ctt gga aat atc tta aaa gaa agg aat gag cta cag gaa gct			1588
Asn Asn Leu Gly Asn Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala			
430	435	440	
gag gag ctg ctg tct ttg gct gtt caa ata cag cca gac ttt gcc gct			1636
Glu Glu Leu Leu Ser Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala			
445	450	455	
gcg tgg atg aat cta ggc ata gtg cag aat agc ctg aaa cgg ttt gaa			1684
Ala Trp Met Asn Leu Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu			
460	465	470	475
gca gca gag caa agt tac cgg aca gca att aaa cac aga agg aaa tac			1732

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Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr	
480 485 490	
cca gac tgt tac tac aac ctc ggg cgt ctg tat gca gat ctc aat cgc	1780
Pro Asp Cys Tyr Tyr Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg	
495 500 505	
cac gtg gat gcc ttg aat gcg tgg aga aat gcc acc gtg ctg aaa cca	1828
His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro	
510 515 520	
gag cac agc ctg gcc tgg aac aac atg att ata ctc ctc gac aat aca	1876
Glu His Ser Leu Ala Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr	
525 530 535	
ggt aat tta gcc caa gct gaa gca gtt gga aga gag gca ctg gaa tta	1924
Gly Asn Leu Ala Gln Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu	
540 545 550 555	
ata cct aat gat cac tct ctc atg ttc tcg ttg gca aac gtg ctg ggg	1972
Ile Pro Asn Asp His Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly	
560 565 570	
aaa tcc cag aaa tac aag gaa tct gaa gct tta ttc ctc aag gca att	2020
Lys Ser Gln Lys Tyr Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile	
575 580 585	
aaa gca aat cca aat gct gca agt tac cat ggt aat ttg gct gtg ctt	2068
Lys Ala Asn Pro Asn Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu	
590 595 600	
tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc	2116
Tyr His Arg Trp Gly His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile	
605 610 615	
tcc ttg cag ctt gac ccc acg gca tca gga act aag gag aat tac ggt	2164
Ser Leu Gln Leu Asp Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly	
620 625 630 635	
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tgat	2210
Leu Leu Arg Arg Lys Leu Glu Leu Met Gln Lys Lys Ala Val	
640 645	
cctgtttcct tcatgttttg agtttgagtg tgtgtgtgca tgaggcatat cattaatagt	2270
atgtggttac atttaaccat ttaaaagtct tagacatggt attttactga tttttttcta	2330
tgaaaacaaa gacatgcaaa aagattatag caccagcaat atactcttga atgcgtgata	2390

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tgatttttca ttgaaattgt attttttcag acaactcaaa tgtaattcta aaattccaaa 2450
aatgtctttt ttaattaaac agaaaaagag aaaaaattat cttgagcaac ttttagtaga 2510
attgagctta catttgggat ctgagccttg tctgtatgg actagcacta ttaaacttca 2570
attatgacca agaaaggata cactggcccc tacaatttgt ataaatattg aacatgtcta 2630
tatattagca tttttattta atgacaaagc aaattaagtt tttttatctc ttttttttaa 2690
aacaacatac tgtgaacttt gtaaggaaat atttatttgt atttttatgt tttgaatagg 2750
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ttcggggaat tctgtgtatt ttttaagaatt gagttgttcc tgcgtgtttt tatttgatcc 3170
aaacaatgtt ttgttttgtt cttctctgta tgcgtgtgac ctaatgattt atgcaatctc 3230
tgtaatttct tatgcagtaa aattactaca caaactagc 3269

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<210> 85

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)...(347)

<400> 85

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acagttcttc tggacttctc tggaccacag tctctgcca gacctctgcc agacccagc 60
ccacc atg atc cat ctg ggt cac atc ctc ttc ctg ctt ttg ctc cca gtg 110
      Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Pro Val
          1             5             10             15
gct gca gct cag acg act cca gga gag aga tca tca ctc cct gcc ttt 158
Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe
          20             25             30
tac cct ggc act tca ggc tct tgt tcc gga tgt ggg tcc ctc tct ctg 206
Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu
          35             40             45
ccg ctc ctg gca ggc ctc gtg gct gct gat gcg gtg gca tcc ctg ctc 254

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Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu
 50 55 60
 atc gtg ggg gcg gtg ttc ctg tgc gca cgc cca cgc cgc agc ccc gcc 302
 Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala
 65 70 75
 caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg ggc tgaccc 350
 Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 80 85 90
 tcctgcagct tggacctttg acttctgacc ctctcatcct ggatggtgtg tgggtggcaca 410
 ggaacccccg ccccaacttt tggattgtaa taaaacaatt gaaacacc 458

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1457)

<400> 86

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 tggcagcacc cacgcccgcc cgtccggtgc tgaccacact gctggtgget ctettcggc 179
 atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta cct gtg 227
 Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
 1 5 10 15
 gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac gtc tct 275
 Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
 20 25 30
 gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc ctc tgg 323
 Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
 35 40 45
 agg agg ctg gcc cca gga aag gac gag cag gtc ccc atc cgg gtg gtg 371
 Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
 50 55 60
 cag gtg ctg ggc atg gtg ggc aca gcc ctg ctg gcc tct ctg tgg cac 419

Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His			
65	70	75	80
cat gtg gcc cca gtg gca gga cag ttg cat tct gtg gcc ttc tta gca	467		
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala			
85	90	95	
ctg gcc ttt gtg ctg gca ctg gca tgc tgt gcc tcg aat gtc act ttc	515		
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe			
100	105	110	
ctg ccc ttc ttg agc cac ctg cca cct cgc ttc tta cgg tca ttc ttc	563		
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe			
115	120	125	
ctg ggt caa ggc ctg agt gcc ctg ctg ccc tgc gtg ctg gcc cta gtg	611		
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val			
130	135	140	
cag ggt gtg ggc cgc ctc gag tgc ccg cca gcc ccc atc aac ggc acc	659		
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr			
145	150	155	160
cct ggc ccc ccg ctc gac ttc ctt gag cgt ttt ccc gcc agc acc ttc	707		
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe			
165	170	175	
ttc tgg gca ctg act gcc ctt ctg gtc gct tca gct gct gcc ttc cag	755		
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln			
180	185	190	
ggt ctt ctg ctg ctg ttg ccg cca cca cca tct gta ccc aca ggg gag	803		
Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu			
195	200	205	
tta gga tca ggc ctc cag gtg gga gcc cca gga gca gag gaa gag gtg	851		
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val			
210	215	220	
gaa gag tcc tca cca ctg caa gag cca cca agc cag gca gca ggc acc	899		
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr			
225	230	235	240
acc cct ggt cca gac cct aag gcc tat cag ctt cta tca gcc cgc agt	947		
Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser			
245	250	255	

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gcc tgc ctg ctg ggc ctg ttg gcc gcc acc aac gcg ctg acc aat ggc 995
 Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
 260 265 270
 gtg ctg cct gcc gtg cag agc ttt tcc tgc tta ccc tac ggg cgt ctg 1043
 Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
 275 280 285
 gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc 1091
 Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
 290 295 300
 tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc 1139
 Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
 305 310 315 320
 ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcg ctg 1187
 Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
 325 330 335
 gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg ggg gtg 1235
 Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
 340 345 350
 gtc ctc gtg gtg ctg tcg tgg gtg ctg tgt ctt ggc gtg ttc tcc tac 1283
 Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
 355 360 365
 gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg ccg gca 1331
 Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
 370 375 380
 ttg ctg gca gcc ggc gtg gcc atc cag gtg ggc tct ctg ctc ggc gct 1379
 Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
 385 390 395 400
 gtt gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga 1427
 Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
 405 410 415
 aag gac tgt gca gac ccc tgt gac tcc tgagcctggg caggtgggga ccccg 1480
 Lys Asp Cys Ala Asp Pro Cys Asp Ser
 420 425
 tccccaacac ctgtctttcc ctcaatgctg ccaccatgcc tgagtgcctg cagcccagga 1540
 ggccccgcaca ccgttacact cgtggacacc tacacactcc ataggagatc ctggtctttcc 1600

147/233

aggggtgggca agggcaagga gcaggcttgg agccagggac cagtgggggc tgtagggtaa 1660
 gccctgagc ctgggaccta catgtggttt gcgtaataaa acatttgat tt 1712

<210> 87

<211> 1055

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)...(502)

<400> 87

accgggagggc gcgtggggct tgaggccgag aacggccctt gctgccacca ac atg 55
 Met
 1
 gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg 103
 Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu
 5 10 15
 aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg 151
 Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val
 20 25 30
 tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att 199
 Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile
 35 40 45
 tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa 247
 Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu
 50 55 60 65
 cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga 295
 His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly
 70 75 80
 caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga 343
 Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly
 85 90 95
 ggt tta ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca 391
 Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro
 100 105 110

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aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta 439
 Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu
 115 120 125
 ttg agt ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc 487
 Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly
 130 135 140 145
 tat ctg atg ggt tagagtgcct ttgagaagaa atcagtggat actggatttg c 540
 Tyr Leu Met Gly

tctgtcaat gaagttttaa aggctgtacc aatcctctaa tatgaaatgt ggaaaagaat 600
 gaagagcagc agtaaaagaa atatctagtg aaaaaacagg aagcgtattg aagcttggac 660
 tagaatttct tcttggattt aaagagacaa gtttatcaca gaattttttt tctgtctggc 720
 ctattgctat accaatgatg ttgagtggca ttttcttttt agtttttcat taaaatatat 780
 tccatatcta caactataat atcaaataaa gtgattattt ttacaaccc tcttaacatt 840
 ttttgagat gacatttctg attttcagaa attaacataa aatccagaag caagattccg 900
 taagctgaga actctggaca gttgatcagc tttacctatg gtgctttgcc ttttaactaga 960
 gtgtgtgatg gtagattatt tcagatatgt atgtaaaact gtttcttgaa caataagatg 1020
 tatgaacgga gcagaaataa atactttttc taatt 1055

<210> 88

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)...(1412)

<400> 88

gagctctcac ggtttctctt ttctgacaa aaagaatatt aatgaaactt tatcatcttg 60
 gtgagaaaag cattctaata gctttattct gacatacgga ggtatggaga gottgaagga 120
 gtcagagagg tgcccagcta agacctgaat gccatcacc tcccagggc totgcagttt 180
 tctcgtggtg aaccottgat ggatttggtg ttgcttgaga a atg gcg atg atc 233
 Met Ala Met Ile

1

gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt 281
 Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser

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5	10	15	20	
tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta ttt				329
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe				
25	30	35		
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct				377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro				
40	45	50		
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct				425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro				
55	60	65		
gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa ttc				473
Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu Phe				
70	75	80		
cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag aga				521
Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu Arg				
85	90	95	100	
gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc				569
Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile				
105	110	115		
ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg				617
Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp				
120	125	130		
gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt cat				665
Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His				
135	140	145		
gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat tat				713
Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr				
150	155	160		
gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct				761
Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser				
165	170	175	180	
gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac agc				809
Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser				
185	190	195		
gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca				857

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Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala	
200	210
gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag gca cgt	905
Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg	
215	225
ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct	953
Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro	
230	240
gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac tgt	1001
Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys	
245	255
tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt aag	1049
Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys	
265	275
gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg	1097
Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp	
280	290
tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc	1145
Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys	
295	305
gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc	1193
Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe	
310	320
agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc acg	1241
Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile Thr	
325	335
ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat gtg	1289
Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp Val	
345	355
gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc aca	1337
Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu Thr	
360	370
ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg aac	1385
Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu Asn	
375	385

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ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat a 1430
 Leu Leu Gly Lys Arg Lys Thr Arg
 390 395
 aatatcaaag cccaagaaat ggaactttgg gcagagatca tgtagaatc aagtggatga 1490
 tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
 taactgcaaa ataaatagtt gattgtactg ttctcatgt ataaaagtgg acaggtactc 1610
 tacaac 1616

 <210> 89
 <211> 1860
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (69)...(1121)
 <400> 89
 gagaagtgtc gcgtccgtgc gccgcgggct ggggcgggtc caggtgtgcc gaagctctgg 60
 tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107
 Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu
 1 5 10
 agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155
 Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu
 15 20 25
 cag gac aag gag acg gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203
 Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly
 30 35 40 45
 ctg gac agc gag tcc gcc tcc agc agc atc cgc ttc agc aag gcc tgc 251
 Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys
 50 55 60
 ctg aag aac gtc ttc tcg gtc cta ctc atc ttc atc tac ctg ctg ctc 299
 Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu
 65 70 75
 atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347
 Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg
 80 85 90

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gag aaa ctc aag cac cct gtc atg tct gtg tct tac aag gaa gtg gat	395
Glu Lys Leu Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp	
95 100 105	
cgc tat gat gcc cca ggt att gcc ttg tac ccc ggt cag gcc cag ttg	443
Arg Tyr Asp Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu	
110 115 120 125	
ctc agc tgt aag cac cat tac gag gtc att cct cct ctg aca agc cct	491
Leu Ser Cys Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro	
130 135 140	
ggc cag ccg ggt gac atg aat tgc acc acc cag agg atc aac tac acg	539
Gly Gln Pro Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr	
145 150 155	
gac ccc ttc tcc aat cag act gtg aaa tct gcc ctg att gtc cag ggg	587
Asp Pro Phe Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly	
160 165 170	
ccc cgg gaa gtg aaa aag cgg gag ctg gtc ttc ctc cag ttc cgc ctg	635
Pro Arg Glu Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu	
175 180 185	
aac aag agt agt gag gac ttc agc gcc att gat tac ctc ctc ttc tct	683
Asn Lys Ser Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser	
190 195 200 205	
tct ttc cag gag ttc ctg caa agc cca aac agg gta ggc ttc atg cag	731
Ser Phe Gln Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln	
210 215 220	
gcc tgt gag agt gcc tat tcc agc tgg aag ttc tct ggg ggc ttc cgc	779
Ala Cys Glu Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg	
225 230 235	
acc tgg gtc aag atg tca ctg gta aag acc aag gag gag gat ggg cgg	827
Thr Trp Val Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg	
240 245 250	
gaa gca gtg gag ttc cgg cag gag aca agt gtg gtt aac tac att gac	875
Glu Ala Val Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp	
255 260 265	
cag agg cca gct gcc aaa aaa agt gct caa ttg ttt ttt gtg gtc ttt	923
Gln Arg Pro Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe	

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270	275	280	285	
gaa tgg aaa gat cct ttc atc cag aaa gtc caa gat ata gtc act gcc				971
Glu Trp Lys Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala				
290	295	300		
aat cct tgg aac aca att gct ctt ctc tgt ggc gcc ttc ttg gca tta				1019
Asn Pro Trp Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu				
305	310	315		
ttt aaa gca gca gag ttt gcc aaa ctg agt ata aaa tgg atg atc aaa				1067
Phe Lys Ala Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys				
320	325	330		
att aga aag aga tac ctt aaa aga aga ggt cag gca acg agc cac ata				1115
Ile Arg Lys Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile				
335	340	345		
agc tgaagtcacc tcgcgttggt tagagaactg tccacatcaa tgggagctgt ca				1170
Ser				
350				
tcacttccac tttgtaaacg gagctatcaa caatcctgta ctcaacttgaa gaaatggggc				1230
cttgcctggga ggaacagcat gtaaaactgg aacttctaac cccgtcccaa aagaggcggc				1290
gtagagccta atagaagaga ctaatggata aacctacaag ttattttaat atttaaatta				1350
ttaataaaact ttttaaagag ctggccaatg acttttgaat agggtttgta gaagatgcct				1410
ttcttccctgt ttgggttcatt gtattgtatt aggttaagct ctactagggt aatgaaggct				1470
ctacttttca ctttttaaaa gtggacaaaa gagtgtgatt ttctttttcc aaaaattcct				1530
gagtatcaag acgtgcaggt catgctttgg agcctatgca ctgtacacaa aggcaaaacc				1590
ctatgacttt ggcacatct gccattgatg tccagcctct gacatgctct ttgatttggt				1650
aaatgttaaa tgagacttta aggtactag aaactagtaa ttaagtttct taatggactg				1710
agtagccacc tacttgctcg gctagaatgt ttgttgatgt atgagtttag attaacactc				1770
aaaagcacta ggacagatgt acatagaagg tgccactactca ttgtattttg atgatttcat				1830
taacaggtaa ataaaagtta atacaaaagg				1860

<210> 90

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<222> (245)...(706)

<400> 90

acacacccag tgaggtctct ggagccgcgg tgcgggaagc ggggacccgg gtttgaatcc	60
tgccctctctg gtgtggtgcg gcctcttccc acagactttt ggctcagtg ttccccgcct	120
gggaagtggg gactggccct ggtacctggc tccagagctg caccagagg cgatcagccc	180
ggtgcgggaa cggggcgggg tggccgcaac tacgggccac ggatcctgac ccgcctgccc	240
cacg atg act atc cac atc ctc atc ctg ctg ttg ctc ctc gcc ttc	286
Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe	
1 5 10	
tcc gcc caa ggg gac ctg gac act gca gcc agg cga ggc cag cac cag	334
Ser Ala Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln	
15 20 25 30	
gtc ccc cag cac cgc ggg cac gtc tgc tac ctg ggc gta tgc cgg acc	382
Val Pro Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr	
35 40 45	
cac cgc ctg gcg gag atc ata tac tgg att cgc tgt ctc cac caa gga	430
His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly	
50 55 60	
gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg	478
Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp	
65 70 75	
gcg ccg ccg gtg gcg cga ggc gga agc ccg gct cgg ttc cca gga ttc	526
Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe	
80 85 90	
cgg cct gca gcg agg ggg cta gcg cag tgc cca gct cgc tgg gtg acc	574
Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr	
95 100 105 110	
tcg ggc acg gct cgt ccc ctc ctc ggc ttc agt ttg cct atc tgt atg	622
Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met	
115 120 125	
ttg gag ctt cta ctc cac att tct tct ccc cta act cca gcc cct gaa	670
Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu	
130 135 140	
acc gtc ttc ccc agt ccc tcc ccg ggc tgc gac taggttgac ctagaag	720
Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp	

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145

150

cacacgggac caggctgggc gaagaacact gacgccccaga gccgaataaa caagagttcc 780
gtg 783

<210> 91

<211> 303

<212> PRT

<213> Homo sapiens

<400> 91

Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
1 5 10 15
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
20 25 30
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
35 40 45
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
50 55 60
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
65 70 75 80
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
85 90 95
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
100 105 110
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
115 120 125
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
130 135 140
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
145 150 155 160
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
165 170 175
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
180 185 190
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
195 200 205

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Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300

<210> 92

<211> 283

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser
 1 5 10 15
 Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
 20 25 30
 Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
 35 40 45
 Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
 50 55 60
 Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
 65 70 75 80
 Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
 85 90 95
 Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
 100 105 110
 Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
 115 120 125
 Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu

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130 135 140
 Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
 145 150 155 160
 Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser
 165 170 175
 Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
 180 185 190
 Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
 195 200 205
 Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
 210 215 220
 Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
 225 230 235 240
 Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
 245 250 255
 Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
 260 265 270
 Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
 275 280

<210> 93

<211> 488

<212> PRT

<213> Homo sapiens

<400> 93

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
 1 5 10 15
 Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys
 20 25 30
 Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
 35 40 45
 Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
 50 55 60
 Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
 65 70 75 80

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Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
 85 90 95
 Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
 100 105 110
 Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
 115 120 125
 Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
 130 135 140
 Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
 145 150 155 160
 Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
 165 170 175
 Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
 180 185 190
 Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg
 195 200 205
 Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr
 210 215 220
 Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly
 225 230 235 240
 Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly
 245 250 255
 Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu
 260 265 270
 Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr
 275 280 285
 His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu
 290 295 300
 Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu
 305 310 315 320
 Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys
 325 330 335
 Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu
 340 345 350
 Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe

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355 360 365
 Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro
 370 375 380
 Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr
 385 390 395 400
 Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys
 405 410 415
 Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile
 420 425 430
 Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His
 435 440 445
 Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu
 450 455 460
 Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu
 465 470 475 480
 Leu Glu Arg Leu Pro Arg Pro Ser
 485

<210> 94

<211> 182

<212> PRT

<213> Homo sapiens

<400> 94

Met Trp Pro Pro Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly
 1 5 10 15
 Gly Ser Arg Pro Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro
 20 25 30
 Ala Arg Ala Phe Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu
 35 40 45
 Ser Gly Leu Ser Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala
 50 55 60
 Ser Ala Phe Leu Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr
 65 70 75 80
 Phe Leu Phe Ala Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu
 85 90 95

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Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
 100 105 110
 Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
 115 120 125
 Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
 130 135 140
 Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
 145 150 155 160
 Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
 165 170 175
 Ser Asp Ser Asp Ser Asp
 180

<210> 95

<211> 184

<212> PRT

<213> Homo sapiens

<400> 95

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
 1 5 10 15
 Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
 20 25 30
 Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
 35 40 45
 Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
 50 55 60
 Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
 65 70 75 80
 Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
 85 90 95
 Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
 100 105 110
 Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
 115 120 125
 Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

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130 135 140
 Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly
 145 150 155 160
 Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser
 165 170 175
 Gln Thr Pro Gln Pro Lys Asp Lys
 180

<210> 96

<211> 140

<212> PRT

<213> Homo sapiens

<400> 96

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
 1 5 10 15
 Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
 20 25 30
 Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
 35 40 45
 Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
 50 55 60
 Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
 65 70 75 80
 Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe
 85 90 95
 Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met
 100 105 110
 Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu
 115 120 125
 Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
 130 135 140

<210> 97

<211> 153

<212> PRT

162/233

<213> Homo sapiens

<400> 97

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15
 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45
 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60
 His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80
 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95
 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110
 Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125
 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140
 Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150

<210> 98

<211> 173

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Ala Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val
 1 5 10 15
 Gly Val Leu Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu
 20 25 30
 Ile Ser Thr Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu
 35 40 45
 Pro Met Arg Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr

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50 55 60
 Ile Arg Ile Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys
 65 70 75 80
 Phe Met Leu Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser
 85 90 95
 Pro Glu Ser Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro
 100 105 110
 Ser Val Ala Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val
 115 120 125
 Ser Gly Ser Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys
 130 135 140
 Thr Met Gly Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln
 145 150 155 160
 Lys Phe Glu Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170

<210> 99

<211> 75

<212> PRT

<213> Homo sapiens

<400> 99

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1 5 10 15
 Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly
 20 25 30
 Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
 35 40 45
 Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe
 50 55 60
 Met Met Phe Cys Met Ile Val Leu Phe Gly Ser
 65 70 75

<210> 100

<211> 159

<212> PRT

164/233

<213> Homo sapiens

<400> 100

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Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly His Trp
  1             5             10             15
Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp
          20             25             30
Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg
          35             40             45
Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr
          50             55             60
Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser
          65             70             75             80
Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu
          85             90             95
Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu
          100            105            110
Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln
          115            120            125
Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp
          130            135            140
Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr
          145            150            155

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<210> 101

<211> 909

<212> DNA

<213> Homo sapiens

<400> 101

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gcgggtgcctc ccgttgctcc cccgcctgcg accgcggcct caggtccgat ccccaaatct      120
gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggg caacaagtgc      180
tcccttgggg tggtcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca      240
gcggggggcct ggatcatcca cccctacagc gacttcgggt tttactggga cctgatcatg      300
ctgctgctga tgggtgggaa cctcatcgtc ctgcctgtgg gcatcacctt cttcaaggag      360
gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat      420

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ctggtgctca acttccgaac gggcatcgtg gtggaggagg gtgctgagat cctgctggca 480
 ccgcgggcca tccgcacgcg ctacctgcgc acctgggtcc tggttgacct catctcttct 540
 atccctgtgg attacatctt cctagtgggtg gagctggagc cacggttggg cgctgaggtc 600
 tacaaaaacgg cacgggccct acgcatcgtt cgcttcacca agatccctaa cctgctgagg 660
 ctgctccgcc tctccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
 acctatgacc tggccagtgc tgtggttcgc atcttcaacc tcattgggat gatgctgctg 780
 ctatgtcact gggatggctg tctgcagttc ctggtgccc a tgcctgcagga cttccctccc 840
 gactgctggg tctccatcaa ccacatgggtg gtgagaagtc cccacagctc tgcctttcct 900
 gggccttct 909

<210> 102

<211> 849

<212> DNA

<213> Homo sapiens

<400> 102

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 gccacgcggg cacctgggtg cctgagttat cctgcagcct ctcccacgcc ccatgcagcc 120
 ttcttggtg acccgggtgc caacatggcc atggcctatg ggagcagcct ggccgcgcag 180
 ggcaaggagc tgggtggataa gaacatcgac cgcttcatcc ccatcacc aa gctcaagtat 240
 tactttgctg tggacaccat gtatgtgggc agaaagctgg gcctgctgtt cttcccctac 300
 ctacaccagg actgggaagt gcagtaccaa caggacaccc cgggtggccc ccgctttgac 360
 gtcaatgccc cggacctcta cattccagca atggctttca tcacctacgt tttggtggct 420
 ggtcttgccg tggggaccca ggataggttc tcccagacc tcttggggct gcaagcgagc 480
 tcagccctgg cctggctgac cctggagggtg ctggccatcc tgcctcagcct ctatctggtc 540
 actgtcaaca ccgacctcac caccatcgac ctgggtggcct tcttgggcta caaatatgtc 600
 gggatgattg gcggggtcct catgggcctg ctcttcggga agattggcta ctacctggtg 660
 ctgggctggt gctgcgtagc catctttgtg ttcattgatcc ggacgctgcg gctgaagatc 720
 ttggcagacg cagcagctga gggggctccc gtgcgtgggg cccggaacca gctgcgcagt 780
 tacctgacca tggcgtggc ggcggcgcag cctatgctca tgtactggct caccttccac 840
 ctggtgcgg 849

<210> 103

<211> 1464

<212> DNA

<213> Homo sapiens

166/233

<400> 103

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gccactgtcc	acctggtcat	ctgtccctac	accaaagtgg	aggagagctt	caacctgcag	120
gccacacatg	acctgctcta	ccactggcaa	gacctggagc	agtacgacca	tcttgagttc	180
cccggagtcg	tccccaggac	gttcctcggg	ccagtgggtga	tcgcagtgtt	ctccagcccc	240
gcgggtttacg	tgttttcgct	gttagaaatg	tccaagtttt	actctcagct	aatagttaga	300
ggagtgettg	gactcggcgt	gattttttgga	ctctggacgt	tacaaaagga	agtgagacgg	360
cacttcgggg	ccatggtggc	caccatgttc	tgtctgggtga	cggccatgca	gttccacctg	420
atgtttctact	gcacgcggac	actgcccaat	gtgctggccc	tgctgtagt	cctgctggcc	480
ctcgcggcct	ggctgcggca	cgagtgggcc	cgcttcctct	ggctgtcagc	cttcgccatc	540
atcgtgttca	gggtggagct	gtgcctgttc	ctgggcctcc	tgtctgtct	ggccttgggc	600
aaccgaaagg	tttctgtagt	cagagccctt	cggcacgccg	tcccggcagg	gatcctctgt	660
ttaggactga	cggttgctgt	ggactcttat	ttttggcggc	agctcacttg	gccggaagga	720
aaggtgcttt	ggtacaacac	tgtcctgaac	aaaagctcca	actgggggac	ctccccgctg	780
ctgtggtact	tctactcagc	cctgccccgc	ggcctgggct	gcagcctgct	cttcattcccc	840
ctgggcttgg	tagacagaag	gacgcacgcg	ccgacgggtgc	tggcactggg	cttcattggca	900
ctctactccc	tcttgcaca	caaggagcta	cgtttcatca	tctatgcctt	ccccatgctc	960
aacatcacgg	ctgocagagg	ctgtccttac	ctgctgaata	actataaaaa	gtcttggtgtg	1020
tacaaagcag	ggtctctgct	tgtgatcgga	cacctcgtgg	tgaatgccgc	ctactcagcc	1080
acggccctgt	atgtgtccca	tttcaactac	ccaggtggcg	tcgcaatgca	gaggctgcac	1140
cagctggtgc	ccccccagac	agacgtcctt	ctgcacattg	acgtggcagc	cggccagaca	1200
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cagccgggga	caggcatgct	ggcatacaca	cacatcctca	tggaggcggc	ccctgggctc	1320
ctggccctct	acagggacac	acaccgggtc	ctggccagcg	tcgtggggac	cacaggtgtg	1380
agtctgaacc	tgacccaact	gcccccttc	aacgtccacc	tgcagacaaa	gctggtgctt	1440
ctggagaggg	tccccgggcc	gtcc				1464

<210> 104

<211> 546

<212> DNA

<213> Homo sapiens

<400> 104

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ggccccgcgg	tccccgggct	ccgcgccttg	ctgccggcgc	gggetttcct	ctgctctctc	120
aaaggccgcc	tctgtctggc	cgagtcgggt	ctctcattca	tcacttttat	ctgctatgtg	180

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gcgtcctcag catctgcctt cctcacagcg cctctgctgg agttcctgct ggccttgtag	240
ttcctctttg ctgatgccat gcagctgaat gacaagtggc agggcttggt ctggcccatg	300
atggacttcc tgcgctgtgt caccgcggcc ctcatctact ttgctatctc catcacggcc	360
atcgccaagt actcggatgg ggcttccaaa gccgctgggg tgtttggctt ctttgctacc	420
atcgtgtttg caactgattt ctacctgac tttaacgacg tggccaaatt cctcaaacaa	480
ggggactctg cagatgagac cacagcccac aagacagaag aagagaattc cgactcggac	540
tctgac	546

<210> 105

<211> 552

<212> DNA

<213> Homo sapiens

<400> 105

atggacggcc tgaggcagcg cgtggagcac ttctggagc aaaggaacct ggtcaccgaa	60
gtgctggggg cgtggaggg caagaccggg gtggagaagc ggtatctggc tgcaggagcc	120
gtcactctgc taagcctgta tctgctgttc ggctacggag cgtctctgct gtgcaatctc	180
atcggatttg tgtaccccg c atctgcctca atcaaagcta tcgagagccc aagcaaggac	240
gacgacactg tgtggctcac ctactgggtg gtgtacgcc tgtttgggct ggccgagttc	300
ttcagcgatc tactcctgtc ctgggtccct ttctactacg tgggcaagtg cgccttctg	360
ttgttctgca tggctcccag gccctggaac ggggctctca tgetgtatca gcgcgtcgtg	420
cgtccgctgt tctaaggca ccacggggcc gtagacagaa tcatgaacga cctcagcggg	480
cgagccctgg acgcggcggc cggaataacc aggaacgtca agccaagcca gaccccgag	540
ccgaaggaca ag	552

<210> 106

<211> 420

<212> DNA

<213> Homo sapiens

<400> 106

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gggaacacgc tgcagagctt ccgagaccac acttttctct atgaaaagct ctacactggc	120
aagccaaacc ttgtgaatgg cctccaagct cggacctttg ggatctggac gctgctctca	180
tcagtgatte gctgcctctg tgccattgac attcacaaca agacgtctca tcacatcaca	240
ctctggacct tctccttgc cctggggcat ttctctctg agttgtttgt ctatggaact	300
gcagctccca cgattggcgt cctggcacco ctgatggtgg caagtttctc catcctgggt	360

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atgctgggtcg ggctccggtg tctagaagta gaaccagtat ccagacagaa gaagagaaac 420

<210> 107

<211> 459

<212> DNA

<213> Homo sapiens

<400> 107

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 ggtatgtggc tgacatatgc attgggagtt ggcttgettc atattgtctt actcagcatt 120
 cccttcttca gtgttcctgt tgcttggact ttaacaaata ttatacataa tctggggatg 180
 tacgtatttt tgcattgcagt gaaaggaaca cctttcgaaa ctctgacca gggtaaagca 240
 aggtctcctaa ctcatggga acaactggac tatggagtac agtttacatc ttcacggaag 300
 tttttcacaa tttctccaat aattctatat tttctggcaa gtttctatac gaagtatgat 360
 ccaactcaact tcatactaaa cacagcttct ctctgagtg tactaattcc caaatgcca 420
 caactacatg gtgttcggat ctttgaatt aataagtat 459

<210> 108

<211> 519

<212> DNA

<213> Homo sapiens

<400> 108

atgggtgcct tctgataca gaccaaggac aaccccatga aggccgtggg tgtgctggcc 60
 ggcaccatgg ccaccgtcgt ggccatcact gtctcatct ccaccgccac cttctggcgc 120
 aacaagaagt ctaacaaggt cctgccaatg cggcgggtgc tccgcaagcg gccagccct 180
 gcgccccgca ccatccgcat tgagtggctc aagtccaaga gcaccaaaagc cgtaccaag 240
 ttcatgctca aagagaaacc tcccaatgag aactgtaaca acaacagccc agaaagctct 300
 ctgctccgga gagctcggc tctccctcca ccaccagcg tggcgcccag cactggcgca 360
 gccagtgga ccgtgectac tgtctctggc tetctcactc cgcagccgac ccaacccccg 420
 ccaaaaccca aaactatggg aagccccgtc cagtcaactc tgatctctga gctcaagcaa 480
 aagtttgaga agaagagtgt gcacaacaag gcttacttc 519

<210> 109

<211> 225

<212> DNA

<213> Homo sapiens

169/233

<400> 109

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tttaagctga aaaagaagga cacgcagggc tttggggagg agtccagga gccagcaca	120
ggtgacaaca tccgggaatt cttgctgagc ctcagatact ttcgaatctt catcgccctg	180
tggaacatct tcatgatgtt ctgcatgatt gtgctgttcg gctct	225

<210> 110

<211> 477

<212> DNA

<213> Homo sapiens

<400> 110

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tggggctgca ttgtattctc aggetcctat gcctgggcca acttcaccat cctggccttg	120
ggcgtgtggg ctgtggctca gcgggactcc atcgacgcca taagcatgtt tctgggtggc	180
ttgtggcca ccatcttcct ggacatcgtg cacatcagca tcttctaccc gcgggtcagc	240
ctcacggaca cgggcccgtt tggcgtgggc atggccatcc tcagcttget gctcaagccg	300
ctctcctgct gcttcgtcta ccacatgtac cgggagcgcg ggggtgagct cctgggtccac	360
actggtttcc ttgggtcttc tcaggaccgt agtgcctacc agacgattga ctcagcagag	420
gcgcccgcag atccctttgc agtcccagag ggcaggagtc aagatgcccg aggggtac	477

<210> 111

<211> 3438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1032)

<400> 111

gcctacgacg cctccgctag agcccgcggg gctgcgccga ctctgctct ggaggggttg	60
cgggtacctg atggccacag agggctctag gaggccgagc gtgtaagcgg ggtgggcgcc	120
atg gag gca gag cag cgg ccg gcg gcg ggg gcc agc gaa ggg gcg acc	168
Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr	
1 5 10 15	
cct gga ctg gag gcg gtg cct ccc gtt get ccc ccg cct gcg acc gcg	216
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala	

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20	25	30	
gcc tca ggt ccg atc ccc aaa tct ggg cct gag cct aag agg agg cac			264
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His			
35	40	45	
ctt ggg acg ctg ctg cag cct acg gtc aac aag ttc tcc ctt cgg gtg			312
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val			
50	55	60	
ttc ggc agc cac aaa gca gtg gaa atc gag cag gag cgg gtg aag tca			360
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser			
65	70	75	80
gcg ggg gcc tgg atc atc cac ccc tac agc gac ttc cgg ttt tac tgg			408
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp			
85	90	95	
gac ctg atc atg ctg ctg ctg atg gtg ggg aac ctc atc gtc ctg cct			456
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro			
100	105	110	
gtg ggc atc acc ttc ttc aag gag gag aac tcc ccg cct tgg atc gtc			504
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val			
115	120	125	
ttc aac gta ttg tct gat act ttc ttc cta ctg gat ctg gtg ctc aac			552
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn			
130	135	140	
ttc cga acg ggc atc gtg gtg gag gag ggt gct gag atc ctg ctg gca			600
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala			
145	150	155	160
ccg cgg gcc atc cgc acg cgc tac ctg cgc acc tgg ttc ctg gtt gac			648
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp			
165	170	175	
ctc atc tct tct atc cct gtg gat tac atc ttc cta gtg gtg gag ctg			696
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu			
180	185	190	
gag cca cgg ttg gac gct gag gtc tac aaa acg gca cgg gcc cta cgc			744
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg			
195	200	205	
atc gtt cgc ttc acc aag atc cta agc ctg ctg agg ctg ctc cgc ctc			792

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Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu	
210	215
tcc cgc ctc atc cgc tac ata cac cag tgg gag gag atc ttt cac atg	840
Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met	
225	230
acc tat gac ctg gcc agt gct gtg gtt cgc atc ttc aac ctc att ggg	888
Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly	
245	250
atg atg ctg ctg cta tgt cac tgg gat ggc tgt ctg cag ttc ctg gtg	936
Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val	
260	265
ccc atg ctg cag gac ttc cct ccc gac tgc tgg gtc tcc atc aac cac	984
Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His	
275	280
atg gtg gtg aga agt ccc cac agc tct gcc ttt cct ggg cct tct t	1030
Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser	
290	295
agggctcttc tgcctgagta gcagggatgg ccacagggag caggaggtgg gagatgatca	1090
caacagaaaa taggagcgag gaggtgggga ggagggagga aaggggaagg agaccagaa	1150
gaagtgotcg tgtgttgag ggagcaggca aaggaaggg acctaccgga aagctgagga	1210
ccccaaagttg caatagagga cctttttgcc tcagggcccc ccagaaccaa acttaagtgc	1270
ctgccaggag gaaggcctgc agtagaaggg gcagacagaa agaccaaaga aggaaaaggg	1330
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cagaaccact cgtggggccg ccagtattcc catgccctgt tcaaggccat gagccacatg	1450
ctgtgcattg gctatgggca gcaggcacct gtaggcagtc ccgacgtctg gctcaccatg	1510
ctcagcatga tcgtaggtgc cacatgctac gccatgttca tcggccatgc cagggcactc	1570
atccagtccc tggactcttc cgggcgtcag taccaggaga agtacaagca ggtggagcag	1630
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caccgctacc agggcaagat gttcgatgag gaaagcatcc tgggcgagct gagcgagccg	1750
cttcgcgagg agatcattaa cttcacctgt cggggcctgg tggccacat gccgctgttt	1810
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cagccggggg atctcgtggt gcgtgagggc tccgtgggga ggaagatgta cttcatccag	1930
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tactttgggg agatctgctt gctaaactagg ggccggcgca cagccagtgt tcgggctgac	2050
acctactgcc gcctttactc actcagcgtg gaccatttca atgctgtgct tgaggagttc	2110

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atggagcagc acttggtgca acatgacaga gacatggctc ggggtgttcg gggcggggcc 2290
ccgagcacag gagctcagct tagtggaag ccagtactgt gggagccact ggtacatgcg 2350
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<211> 1144

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<220>

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<222> (56)...(907)

<400> 112

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Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser

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1	5	10	15	
egg ggc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca				151
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala				
20	25	30		
gcc tct ccc acg ccc cat gca gcc ttc ctg gct gac ccg gtg tcc aac				199
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn				
35	40	45		
atg gcc atg gcc tat ggg agc agc ctg gcc gcg cag ggc aag gag ctg				247
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu				
50	55	60		
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctc aag tat				295
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr				
65	70	75	80	
tac ttt gct gtg gac acc atg tat gtg ggc aga aag ctg ggc ctg ctg				343
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu				
85	90	95		
ttc ttc ccc tac cta cac cag gac tgg gaa gtg cag tac caa cag gac				391
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp				
100	105	110		
acc ccg gtg gcc ccc cgc ttt gac gtc aat gcc ccg gac ctc tac att				439
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile				
115	120	125		
cca gca atg gct ttc atc acc tac gtt ttg gtg gct ggt ctt gcg ctg				487
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu				
130	135	140		
ggg acc cag gat agg ttc tcc cca gac ctc ctg ggg ctg caa gcg agc				535
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser				
145	150	155	160	
tca gcc ctg gcc tgg ctg acc ctg gag gtg ctg gcc atc ctg ctc agc				583
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser				
165	170	175		
ctc tat ctg gtc act gtc aac acc gac ctc acc acc atc gac ctg gtg				631
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val				
180	185	190		
gcc ttc ttg ggc tac aaa tat gtc ggg atg att ggc ggg gtc ctc atg				679

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Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met	
195 200 205	
ggc ctg ctc ttc ggg aag att ggc tac tac ctg gtg ctg ggc tgg tgc	727
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys	
210 215 220	
tgc gta gcc atc ttt gtg ttc atg atc cgg acg ctg cgg ctg aag atc	775
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile	
225 230 235 240	
ttg gca gac gca gca gct gag ggg gtc ccg gtg cgt ggg gcc cgg aac	823
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn	
245 250 255	
cag ctg cgc atg tac ctg acc atg gcg gtg gcg gcg gcg cag cct atg	871
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met	
260 265 270	
ctc atg tac tgg ctc acc ttc cac ctg gtg cgg tgagcgcgcc cgctga	920
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg	
275 280	
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tgcaggcccc aaggtccacc ctgtctggcc acaggcaccg cctccatccc atgtcccgcc	1040
cagccccgcc cccaaccxaa ggtgctgaga gatctccagc tgcacaggcc accgccccag	1100
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ccgaggctgg ccaggcagc cgcgcttcga aggacgccgc cgggagctgc ggagcatgcg	180
tggagtggca gtgctaacgg ctggtgtctc gcactgttgg cctgtgaagg tacgtgaagc	240
tgaagcctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg	288

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Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu																
1			5			10										
ctg	ctg	ggg	ctg	ctg	gtg	gcc	gta	gcc	act	gtc	cac	ctg	gtc	atc	tgt	336
Leu	Leu	Gly	Leu	Leu	Val	Ala	Val	Ala	Thr	Val	His	Leu	Val	Ile	Cys	
15			20			25										
ccc	tac	acc	aaa	gtg	gag	gag	agc	ttc	aac	ctg	cag	gcc	aca	cat	gac	384
Pro	Tyr	Thr	Lys	Val	Glu	Glu	Ser	Phe	Asn	Leu	Gln	Ala	Thr	His	Asp	
30			35			40										
ctg	ctc	tac	cac	tgg	caa	gac	ctg	gag	cag	tac	gac	cat	ctt	gag	ttc	432
Leu	Leu	Tyr	His	Trp	Gln	Asp	Leu	Glu	Gln	Tyr	Asp	His	Leu	Glu	Phe	
45			50			55				60						
ccc	gga	gtc	gtc	ccc	agg	acg	ttc	ctc	ggg	cca	gtg	gtg	atc	gca	gtg	480
Pro	Gly	Val	Val	Pro	Arg	Thr	Phe	Leu	Gly	Pro	Val	Val	Ile	Ala	Val	
65			70			75										
ttc	tcc	agc	ccc	gcg	gtt	tac	gtg	ctt	tgc	ctg	tta	gaa	atg	tcc	aag	528
Phe	Ser	Ser	Pro	Ala	Val	Tyr	Val	Leu	Ser	Leu	Leu	Glu	Met	Ser	Lys	
80			85			90										
ttt	tac	tct	cag	cta	ata	gtt	aga	gga	gtg	ctt	gga	ctc	ggc	gtg	att	576
Phe	Tyr	Ser	Gln	Leu	Ile	Val	Arg	Gly	Val	Leu	Gly	Leu	Gly	Val	Ile	
95			100			105										
ttt	gga	ctc	tgg	acg	tta	caa	aag	gaa	gtg	aga	cgg	cac	ttc	ggg	gcc	624
Phe	Gly	Leu	Trp	Thr	Leu	Gln	Lys	Glu	Val	Arg	Arg	His	Phe	Gly	Ala	
110			115			120										
atg	gtg	gcc	acc	atg	ttc	tgc	tgg	gtg	acg	gcc	atg	cag	ttc	cac	ctg	672
Met	Val	Ala	Thr	Met	Phe	Cys	Trp	Val	Thr	Ala	Met	Gln	Phe	His	Leu	
125			130			135				140						
atg	ttc	tac	tgc	acg	cgg	aca	ctg	ccc	aat	gtg	ctg	gcc	ctg	cct	gta	720
Met	Phe	Tyr	Cys	Thr	Arg	Thr	Leu	Pro	Asn	Val	Leu	Ala	Leu	Pro	Val	
145			150			155										
gtc	ctg	ctg	gcc	ctc	gcg	gcc	tgg	ctg	cgg	cac	gag	tgg	gcc	cgc	ttc	768
Val	Leu	Leu	Ala	Leu	Ala	Ala	Trp	Leu	Arg	His	Glu	Trp	Ala	Arg	Phe	
160			165			170										
atc	tgg	ctg	tca	gcc	ttc	gcc	atc	atc	gtg	ttc	agg	gtg	gag	ctg	tgc	816
Ile	Trp	Leu	Ser	Ala	Phe	Ala	Ile	Ile	Val	Phe	Arg	Val	Glu	Leu	Cys	
175			180			185										

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ctg ttc ctg ggc ctc ctg ctg ctg ctg gcc ttg ggc aac cga aag gtt	864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val	
190 195 200	
tct gta gtc aga gcc ctt cgc cac gcc gtc ccg gca ggg atc ctc tgt	912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys	
205 210 215 220	
tta gga ctg acg gtt gct gtg gac tct tat ttt tgg cgg cag ctc act	960
Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr	
225 230 235	
tgg ccg gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc	1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser	
240 245 250	
tcc aac tgg ggg acc tcc ccg ctg ctg tgg tac ttc tac tca gcc ctg	1056
Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu	
255 260 265	
ccc cgc ggc ctg ggc tgc agc ctg ctc ttc atc ccc ctg ggc ttg gta	1104
Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val	
270 275 280	
gac aga agg acg cac gcg ccg acg gtg ctg gca ctg ggc ttc atg gca	1152
Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	
285 290 295 300	
ctc tac tcc ctc ctg cca cac aag gag cta cgc ttc atc atc tat gcc	1200
Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala	
305 310 315	
ttc ccc atg ctc aac atc acg gct gcc aga ggc tgc tcc tac ctg ctg	1248
Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu	
320 325 330	
aat aac tat aaa aag tct tgg ctg tac aaa gca ggg tct ctg ctt gtg	1296
Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val	
335 340 345	
atc gga cac ctc gtg gtg aat gcc gcc tac tca gcc acg gcc ctg tat	1344
Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr	
350 355 360	
gtg tcc cat ttc aac tac cca ggt ggc gtc gca atg cag agg ctg cac	1392
Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His	

177/233

365	370	375	380	
cag ctg gtg ccc ccc cag aca gac gtc ctt ctg cac att gac gtg gca				1440
Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala				
	385	390	395	
gcc gcc cag aca ggt gtg tct cgg ttt ctc caa gtc aac agc gcc tgg				1488
Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp				
	400	405	410	
agg tac gac aag agg gag gat gtg cag ccg ggg aca ggc atg ctg gca				1536
Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala				
	415	420	425	
tac aca cac atc ctc atg gag gcg gcc cct ggg ctc ctg gcc ctc tac				1584
Tyr Thr His Ile Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr				
	430	435	440	
agg gac aca cac cgg gtc ctg gcc agc gtc gtg ggg acc aca ggt gtg				1632
Arg Asp Thr His Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val				
	445	450	455	460
agt ctg aac ctg acc caa ctg ccc ccc ttc aac gtc cac ctg cag aca				1680
Ser Leu Asn Leu Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr				
	465	470	475	
aag ctg gtg ctt ctg gag agg ctc ccc cgg ccg tcc tgagggggac cagg				1730
Lys Leu Val Leu Leu Glu Arg Leu Pro Arg Pro Ser				
	480	485		
cagccctcag cagccacagg ccttccagga gctgttatca ctaccagttt ctggcacaat				1790
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gaacgagggg cccagggtctt gttggcaccc cgggagccac tgcccagggt gatggtggcc				1970
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tgccaccact gcaacttttg tattcacagg catcccatct ccatcacaga taaaatctta				2270
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gaacctctc				2339

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178/233

<211> 1756

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<222> (102)...(650)

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Met Trp Pro Pro

1

gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc 161

Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro

5

10

15

20

ggc ccc gcg gtc ccc ggg ctc cgc gcc ctg ctg ccg gcg cgg gct ttc 209

Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe

25

30

35

ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tgc ggt ctc tca 257

Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser

40

45

50

ttc atc act ttt atc tgc tat gtg gcg tcc tca gca tct gcc ttc ctc 305

Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu

55

60

65

aca gcg cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct 353

Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala

70

75

80

gat gcc atg cag ctg aat gac aag tgg cag ggc ttg tgc tgg ccc atg 401

Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu Cys Trp Pro Met

85

90

95

100

atg gac ttc ctg cgc tgt gtc acc gcg gcc ctc atc tac ttt gct atc 449

Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile

105

110

115

tcc atc acg gcc atc gcc aag tac tgc gat ggg gct tcc aaa gcc gct 497

Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala

120

125

130

179/233

ggg gtg ttt ggc ttc ttt gct acc atc gtg ttt gca act gat ttc tac 545
 Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
 135 140 145
 ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggg gac tct gca 593
 Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln Gly Asp Ser Ala
 150 155 160
 gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tcg gac 641
 Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
 165 170 175 180
 tct gac tgaaggcctg gcgggtgcct tggcaacctg agccacacag gcc 690
 Ser Asp

tccacccttg cgcctcacag gggtcgctgg cgttgagcgc gaggcctgga cttctgagtt 750
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<211> 1418

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<213> Homo sapiens

180/233

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<221> CDS

<222> (149)...(703)

<400> 115

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agcagccaac cccggggcgcg tcgggggcc atg gac ggc ctg agg cag cgc gtg      172
                               Met Asp Gly Leu Arg Gln Arg Val
                               1             5

gag cac ttc ctg gag caa agg aac ctg gtc acc gaa gtg ctg ggg gcg      220
Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
      10             15             20

ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc      268
Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
      25             30             35             40

gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga gcg tct ctg      316
Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
      45             50             55

ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat gcc tca atc aaa      364
Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
      60             65             70

gct atc gag agc cca agc aag gac gac gac act gtg tgg ctc acc tac      412
Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
      75             80             85

tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc ttc agc gat cta      460
Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
      90             95             100

ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag tgc gcc ttc ctg      508
Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
      105             110             115             120

ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctc atg ctg tat      556
Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
      125             130             135

cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggg gcc gta gac      604
Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp

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181/233

140	145	150	
aga atc atg aac gac ctc agc ggg cga gcc ctg gac gcg gcg gcc gga			652
Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp Ala Ala Gly			
155	160	165	
ata acc agg aac gtc aag cca agc cag acc ccg cag ccg aag gac aag			700
Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln Pro Lys Asp Lys			
170	175	180	
tgaagcagcc ccctgagcct cacaaggacc tcctggctgg tgaggagggg gccgcgccag			760
gctcccaggc ctccacagag tottcagcgc atcccccaac agcagcccct gccagtccct			820
cgggtccagg caaggccctg ggggtctcct taaatgccac ctcgggcaag tcccagtcct			880
agtcctcggc cccccccage totggatccc agggccagct gccctctggc tctggctgtg			940
gctcccgcct gtccggcagg gcccagggcc agcgtcgggc acagggcagc tccactgggt			1000
ctcggaacaa caccagccg cctggtactt cctccggccc ctcccagtca gccctcccgt			1060
cctcggggcc cctgcagcca cccaacgtca cctccagccc ggtctcacc atggtccagt			1120
ctcccagcag cagcaacatc cccacgcagc ccccagcaa gtcctctggc aagccggagg			1180
acgcagcccc caagaccagc ggacagcgcc agaaggaatc gtcgaaacag cctgccagca			1240
gcgcctcagt gcccgagctg gtcccctgcc attccgggac ctctctggag tacacttcgg			1300
agtccaccac cgagatcacc tgcagctggc cacaccacag gcccccgctc ctgcagcact			1360
actggtgcct gaaacacctg gcctgctagg aggtccaat aaagctaacc cggaccag			1418

<210> 116

<211> 1211

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)...(555)

<400> 116

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ggctgctgct gccactgctg tgetgggggc ccggtcgcca ggcaaaaagc cctcccacgt	120
ttgaggggag tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg	168

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu

1

5

10

gtt atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga	216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg	

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15	20	25	
gac cac act ttt ctc tat gaa aag ctc tac act ggc aag cca aac ctt			264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu			
30	35	40	
gtg aat ggc ctc caa gct cgg acc ttt ggg atc tgg acg ctg ctc tca			312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser			
45	50	55	60
tca gtg att cgc tgc ctc tgt gcc att gac att cac aac aag acg ctc			360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu			
65	70	75	
tat cac atc aca ctc tgg acc ttc ctc ctt gcc ctg ggg cat ttc ctc			408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu			
80	85	90	
tct gag ttg ttt gtc tat gga act gca gct ccc acg att ggc gtc ctg			456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu			
95	100	105	
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg			504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly			
110	115	120	
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac			552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn			
125	130	135	140
tgaggcca gcattatcac ctccaggact ttctcgtttt ccaccttgge catcttcttc			610
cttcgtcgtc tctcctcttt aatttctttt ctattccatc atctgccctt ttattcactt			670
ttagcctctt tttttaattt ttaaaattta aagatatgca tactgaaaag tatataacat			730
gtacgtacaa tttaagaat aattttaag tgaatactac gtaactccat ccaagtcaag			790
aaattgccag cttctcggaa gccactgtg tctccttccc ctacctgcaa cctcttccag			850
gtccctcttt ccagccttcc cctttttccc ttttattttc atgccttgat ttgacttggt			910
tggtgggaac atgtgaacta tgaaacttaa acctgctgcc caccagagc agctgtgacc			970
aagggtgcc tcaaggggtt gtccacgcag gttgggtccc tctctgctgc tggacccaag			1030
actctgaacc ttccaaggga caggcagttc ttctaagaag ggctcccctg tgtgtgagca			1090
agaccacagc tctccttcta tctacagatg catgaggggtt ggaagagtct gggctgtttt			1150
tagaccttct ggtcagctgt atttgtgtaa caacttttgt aataaataga aaaaccctct			1210
g			1211

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<210> 117

<211> 1099

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)...(644)

<400> 117

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ggcggcatgt accttcacac ttgagtattc agaaagaagt gatctgaact ctgaccattc      120
tttatggata cattaagtca aatataagag tctgactact tgacacactg gctcgagcaa      180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt      227
    Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg
      1             5             10             15
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc      275
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly
      20             25             30
ttg ctt cat att gtc tta ctc agc att ccc ttc ttc agt gtt cct gtt      323
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val
      35             40             45
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt      371
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe
      50             55             60
ttg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa      419
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
      65             70             75
gca agg ctc cta act cat tgg gaa caa ctg gac tat gga gta cag ttt      467
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe
      80             85             90             95
aca tct tca cgg aag ttt ttc aca att tct cca ata att cta tat ttt      515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe
      100            105            110
ctg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac      563
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn
      115            120            125

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aca gct tct ctc ctg agt gta cta att ccc aaa atg cca caa cta cat 611
 Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His

130

135

140

ggc gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga 660
 Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr

145

150

aaaaaaattt tacagctact gaattttotta taaggaagga gtggttagta aactgcactg 720
 tttctctgat aatgtgaaat gagaagtatt tacattggag ggccaatggc tggccttca 780
 agtgctgttt tgaagtgcag atttccatta aatgatgcct ctgtttaata cacctggtac 840
 atttctgaag aggggcttta taagcagget gggcaggccc agcttataag ttaaagggea 900
 tcacagtgcg ggtgtagtag ataaattcaa ggaaataaga gatttgtaag aaactaggac 960
 cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc 1020
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<210> 118

<211> 3489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227)...(748)

<400> 118

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 aaaagcccat agtgcctatc agattctcaa agggactcct gactccagaa agtttaaaaa 120
 ccattagget taaggaagca catacctact ctgtactcca gggaccaggt gggaacagct 180
 gagtgcaggg agtggctttc tctttcagac cctctcccgg agcccc atg gct gcc 235

Met Ala Ala

1

ttc ctg ata cag acc aag gac aac ccc atg aag gcc gtg ggt gtg ctg 283
 Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val Gly Val Leu

5

10

15

gcc gcc acc atg gcc acc gtc gtg gcc atc act gtc ctc atc tcc acc 331
 Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu Ile Ser Thr

20

25

30

35

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gcc acc ttc tgg cgc aac aag aag tct aac aag gtc ctg cca atg cgg 379
 Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu Pro Met Arg
 40 45 50
 cgg gtg ctc cgc aag cgg ccc agc cct gcg ccc cgc acc atc cgc att 427
 Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr Ile Arg Ile
 55 60 65
 gag tgg ctc aag tcc aag agc acc aaa gcc gct acc aag ttc atg ctc 475
 Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys Phe Met Leu
 70 75 80
 aaa gag aaa cct ccc aat gag aac tgt aac aac aac agc cca gaa agc 523
 Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser Pro Glu Ser
 85 90 95
 tct ctg ctc ccg aga gct ccg gct ctc cct cca cca ccc agc gtg gcg 571
 Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro Ser Val Ala
 100 105 110 115
 ccc agc act ggc gca gcc cag tgg acc gtg cct act gtc tct ggc tct 619
 Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val Ser Gly Ser
 120 125 130
 ctc act ccg cag ccg acc caa ccc ccg cca aaa ccc aaa act atg gga 667
 Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys Thr Met Gly
 135 140 145
 agc ccc gtc cag tca act ctg atc tct gag ctc aag caa aag ttt gag 715
 Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln Lys Phe Glu
 150 155 160
 aag aag agt gtg cac aac aag gct tac ttc tagtgtatgc cctat 760
 Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170
 gaccccccat ctttctccg cccctgaccc ccaccaccct gctgctcgga ctatgctccc 820
 ctctctctgc tccttaaggt cactgacccc tgttttgac aatggtataa tccccactgt 880
 cctcatctct accgccacct totggcgcaa caagaagttg cgctctgaca gggctctagt 940
 cagggccttg ggcaagacat tgggctctag gatgcaattg gcaaatacgt ccccgttact 1000
 caaatccttg gcactactac aatgccctcc attcttcagg gctgagaatt gacgagaagc 1060
 cagctcacc atcccagacc tcacagtccc tcaggttcta ctgggatctc atcatcatcc 1120
 ttagtcaagc agcagggccc tggccacgtg gagcaacact gactagaatc tggatcctga 1180
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cagcgaacct	cgtgggctgt	aggaaagcaa	atgtaggtaa	ggggagagca	aggatgcaca	1300
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ccttgggaaa	gctgtttaaa	gtcgtctgac	atcctcttcc	tcactctgtaa	atgaagaaag	1720
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gcaggcactg	tgctgggctt	aggggctacc	actggatgat	ggcattgccg	tgactcacac	1960
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gcacagagag	agaaaagtag	aacagttctt	tgcatttggc	tctacttact	aacaaccctt	2320
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gccatggatg	gggaagtgcc	cggtagccag	catgagccac	actaggaaag	aggaggaggg	3220
tgcagccaaa	cttaaggcac	cggcaagtgt	tgtcagcact	ggaggagacc	ccgccagtgg	3280
ggtgaggcca	gccaaagccc	tgtgttacga	atggtggggc	aaggggctgt	ctgctaggtc	3340

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cagtaggaca ggcagagctc caggctggca ccatggtagg cctccaggga aagagctggg 3400
 aggcaggaat ggcacactgg gcaggcttgc ccattcctgg ccctgagaat ggagctgtag 3460
 cctcatggac aataaatgga tgtgacacc 3489

<210> 119

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)...(252)

<400> 119

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Met Ile Gly Asp Ile Leu Leu Phe Gly

1

5

acg ttg ctg atg aat gcc ggg gcg gtg ctg aac ttt aag ctg aaa aag 99

Thr Leu Leu Met Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys

10

15

20

25

aag gac acg cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt 147

Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly

30

35

40

gac aac atc cgg gaa ttc ttg ctg agc ctc aga tac ttt cga atc ttc 195

Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe

45

50

55

atc gcc ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc 243

Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe

60

65

70

ggc tct tgaatcccag cgatgaaacc aggaactcac tttcccgga tgccgagtct c 300

Gly Ser

75

cattcctcca ttctgatga ctccaagaat gtttttgacc agaaaaccga caaccttccc 360

agaaagtcca agtcgtggt ggggtgaaaa gtgttcgccca aggtgtgcat ggtttcccag 420

ccacgtccct gttttcaaag atagtttcac tttggtctct gaattgaaat gctgtctact 480

gaaagggttt caggagcgtt tatgtaagg gctgtgatga aattgcattc cccatagata 540

aaagaaaaat catttctatc cagagatctg agcagaagga ttggcttggt agtttaacac 600

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agccgtgttt ttggacattc agtggtactt gctgagtctg acagcctctg ggcccggcca 660
 ggggccctgt taacaaactg ctttcacatc ccaacagggt ctgcttgccc actcagtgca 720
 gctgcgatta accctaaagg ctttaaggaa cggggccacct gtaacagaga caccagcctt 780
 cctgtataga cactaaattg ttagcaagag tgttgagcta gttcctgggt aagtgtttcc 840
 acagaagaca tgtggagcag ttgtggggat attaagggaa actttcctct gccttgaccc 900
 ctttggttaa taaaatgact ttgggagcca t 931

<210> 120

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)...(547)

<400> 120

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 Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
 1 5 10
 cac tgg ctg ctg aca acc tgg ggc tgc att gta ttc tca ggc tcc tat 157
 His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
 15 20 25 30
 gcc tgg gcc aac ttc acc atc ctg gcc ttg ggc gtg tgg gct gtg gct 205
 Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
 35 40 45
 cag egg gac tcc atc gac gcc ata agc atg ttt ctg ggt ggc ttg ctg 253
 Gln Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
 50 55 60
 gcc acc atc ttc ctg gac atc gtg cac atc agc atc ttc tac ccg egg 301
 Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
 65 70 75
 gtc agc ctc acg gac acg ggc cgc ttt ggc gtg ggc atg gcc atc ctc 349
 Val Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
 80 85 90
 agc ttg ctg ctc aag ccg ctc tcc tgc tgc ttc gtc tac cac atg tac 397

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Ser Leu Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr
 95 100 105 110
 cgg gag cgc ggg ggt gag ctc ctg gtc cac act ggt ttc ctt ggg tct 445
 Arg Glu Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser
 115 120 125
 tct cag gac cgt agt gcc tac cag acg att gac tca gca gag gcg ccc 493
 Ser Gln Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro
 130 135 140
 gca gat ccc ttt gca gtc cca gag ggc agg agt caa gat gcc cga ggg 541
 Ala Asp Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly
 145 150 155
 tac tgaagccagc cacgctgcgc ccggccctgc cccgggcctt cctcgtgcct gggagg 600
 Tyr

 tcgttctagg gatgctcctg acctccgtct cttggacctt agatggaatg tgtccccagc 660
 tcagggattg cctgaaccaa gaggccagga gcccccatgg gccgcccagt accatgcaca 720
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 tggaaccagg gtctctcttt acctcctacc ccatgggtggc accacagagg ccctcagccg 840
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 cccccaagtt tgctgggctt tgggtggaagc cctgagagct tcaggctcctg ctcagcccga 960
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 agggatgcag ggctggaggc cagaggtgtc agcaacactg tgaccaccca caacctccag 1080
 cctccctttt cagagcacag cattaaagtt tggggaattc tgt 1123

<210> 121

<211> 636

<212> PRT

<213> Homo sapiens

<400> 121

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
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 Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
 20 25 30
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45

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Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
 50 55 60
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
 115 120 125
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
 130 135 140
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys

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	325		330		335
Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly					
340		345		350	
Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile					
355		360		365	
Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro					
370		375		380	
Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu					
385		390		395	400
Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu					
405		410		415	
Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu					
420		425		430	
Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His					
435		440		445	
Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp					
450		455		460	
Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val					
465		470		475	480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn					
485		490		495	
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp					
500		505		510	
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser					
515		520		525	
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro Glu Thr					
530		535		540	
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr					
545		550		555	560
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val					
565		570		575	
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln					
580		585		590	
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln					
595		600		605	

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Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 122

<211> 318

<212> PRT

<213> Homo sapiens

<400> 122

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala

193/233

195	200	205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly		
210	215	220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val		
225	230	235
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe		
245	250	255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu		
260	265	270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His		
275	280	285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg		
290	295	300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp		
305	310	315

<210> 123

<211> 82

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val		
1	5	10
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly		
20	25	30
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile		
35	40	45
Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg		
50	55	60
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu		
65	70	75
Phe Gly		80

<210> 124

194/233

<211> 247

<212> PRT

<213> Homo sapiens

<400> 124

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
 1 5 10 15
 Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
 20 25 30
 Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
 35 40 45
 Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
 50 55 60
 Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
 65 70 75 80
 Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
 85 90 95
 Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
 100 105 110
 Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
 115 120 125
 Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
 130 135 140
 Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
 145 150 155 160
 Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
 165 170 175
 Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
 180 185 190
 Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
 195 200 205
 Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
 210 215 220
 Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 225 230 235 240
 Ser Val Ala Asn Ile Met Pro

195/233

245

<210> 125

<211> 206

<212> PRT

<213> Homo sapiens

<400> 125

Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg Glu Asp Glu Lys
 1 5 10 15
 Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys Asp Thr Glu Asn
 20 25 30
 Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala Leu Leu Leu Leu
 35 40 45
 Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala Ser Phe Ala Leu
 50 55 60
 Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala Val Lys Leu Gly
 65 70 75 80
 Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly Gly Leu Gly Gly
 85 90 95
 Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys Gly Val Leu Ala
 100 105 110
 Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg Val Thr Arg Leu
 115 120 125
 Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly Arg Arg Leu Leu
 130 135 140
 Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly Gly Met Gly Glu
 145 150 155 160
 Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala Ala Trp Gly Val
 165 170 175
 Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu Gly Gly Trp Gly
 180 185 190
 Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys Asp Leu
 195 200 205

<210> 126

196/233

<211> 432

<212> PRT

<213> Homo sapiens

<400> 126

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

197/233

245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu		
260	265	270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp		
275	280	285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe		
290	295	300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu		
305	310	315
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu		
325	330	335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln		
340	345	350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr		
355	360	365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu		
370	375	380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val		
385	390	395
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys		
405	410	415
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val		
420	425	430

<210> 127

<211> 306

<212> PRT

<213> Homo sapiens

<400> 127

Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys		
1	5	10
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala		
20	25	30
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly		
35	40	45

198/233

Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly
 50 55 60
 Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
 65 70 75 80
 Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
 85 90 95
 Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
 100 105 110
 Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
 115 120 125
 Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
 130 135 140
 Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
 145 150 155 160
 Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
 165 170 175
 Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
 180 185 190
 Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala Ser Gln Ala Ala
 195 200 205
 Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys Arg Pro Ala Thr
 210 215 220
 Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp Trp Ala Ser Leu
 225 230 235 240
 Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala Ala Trp Ala Ser
 245 250 255
 Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val Glu Asn Gly Leu
 260 265 270
 Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly Pro Gly Leu Thr
 275 280 285
 Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu Gly Pro Leu Gly
 290 295 300
 Val Arg
 305

199/233

<210> 128

<211> 555

<212> PRT

<213> Homo sapiens

<400> 128

Met Gln Ser Cys Glu Ser Ser Gly Asp Ser Ala Asp Asp Pro Leu Ser
 1 5 10 15
 Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg Val Val Val Ile Gly Ala
 20 25 30
 Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala Leu Leu Glu Gln Gly Phe
 35 40 45
 Thr Asp Val Thr Val Leu Glu Ala Ser Ser His Ile Gly Gly Arg Val
 50 55 60
 Gln Ser Val Lys Leu Gly His Ala Thr Phe Glu Leu Gly Ala Thr Trp
 65 70 75 80
 Ile His Gly Ser His Gly Asn Pro Ile Tyr His Leu Ala Glu Ala Asn
 85 90 95
 Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu Arg Ser Val Gly Arg Ile
 100 105 110
 Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys Tyr Leu Thr Asn His Gly
 115 120 125
 Arg Arg Ile Pro Lys Asp Val Val Glu Glu Phe Ser Asp Leu Tyr Asn
 130 135 140
 Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe Arg His Asp Lys Pro Val
 145 150 155 160
 Asn Ala Glu Ser Gln Asn Ser Val Gly Val Phe Thr Arg Glu Glu Val
 165 170 175
 Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp Pro Glu Ala Thr Lys Arg
 180 185 190
 Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu Lys Val Glu Ser Cys Glu
 195 200 205
 Ser Ser Ser His Ser Met Asp Glu Val Ser Leu Ser Ala Phe Gly Glu
 210 215 220
 Trp Thr Glu Ile Pro Gly Ala His His Ile Ile Pro Ser Gly Phe Met
 225 230 235 240

200/233

Arg Val Val Glu Leu Leu Ala Glu Gly Ile Pro Ala His Val Ile Gln
 245 250 255
 Leu Gly Lys Pro Val Arg Cys Ile His Trp Asp Gln Ala Ser Ala Arg
 260 265 270
 Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly Glu Gly Asp His Asn His
 275 280 285
 Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu Glu Pro Arg Gly Gly Arg
 290 295 300
 Trp Asp Glu Asp Glu Gln Trp Ser Val Val Val Glu Cys Glu Asp Cys
 305 310 315 320
 Glu Leu Ile Pro Ala Asp His Val Ile Val Thr Val Ser Leu Gly Val
 325 330 335
 Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg Pro Gly Leu Pro Thr Glu
 340 345 350
 Lys Val Ala Ala Ile His Arg Leu Gly Ile Gly Thr Thr Asp Lys Ile
 355 360 365
 Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly Pro Glu Cys Asn Ser Leu
 370 375 380
 Gln Phe Val Trp Glu Asp Glu Ala Glu Ser His Thr Leu Thr Tyr Pro
 385 390 395 400
 Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly Phe Asp Val Leu Tyr Pro
 405 410 415
 Pro Glu Arg Tyr Gly His Val Leu Ser Gly Trp Ile Cys Gly Glu Glu
 420 425 430
 Ala Leu Val Met Glu Lys Cys Asp Asp Glu Ala Val Ala Glu Ile Cys
 435 440 445
 Thr Glu Met Leu Arg Gln Phe Thr Gly Asn Pro Asn Ile Pro Lys Pro
 450 455 460
 Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser Asn Pro Tyr Phe Arg Gly
 465 470 475 480
 Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser Gly Ala Asp Val Glu Lys
 485 490 495
 Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser Ser Lys Thr Ala Pro Met
 500 505 510
 Gln Val Leu Phe Ser Gly Glu Ala Thr His Arg Lys Tyr Tyr Ser Thr

201/233

515	520	525
Thr His Gly Ala Leu Leu Ser Gly Gln Arg Glu Ala Ala Arg Leu Ile		
530	535	540
Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly Thr		
545	550	555

<210> 129
 <211> 250
 <212> PRT
 <213> Homo sapiens
 <400> 129

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg		
1	5	10
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu		
20	25	30
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser		
35	40	45
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln		
50	55	60
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg		
65	70	75
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu		
85	90	95
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu		
100	105	110
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln		
115	120	125
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn		
130	135	140
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln		
145	150	155
Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu		
165	170	175
Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu		
180	185	190

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Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
 195 200 205
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
 210 215 220
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
 225 230 235 240
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
 245 250

<210> 130

<211> 174

<212> PRT

<213> Homo sapiens

<400> 130

Met Gln Ala Pro Ala Phe Arg Asp Lys Lys Gln Gly Val Ser Ala Lys
 1 5 10 15
 Asn Gln Gly Ala His Asp Pro Asp Tyr Glu Asn Ile Thr Leu Ala Phe
 20 25 30
 Lys Asn Gln Asp His Ala Lys Gly Gly His Ser Arg Pro Thr Ser Gln
 35 40 45
 Val Pro Ala Gln Cys Arg Pro Pro Ser Asp Ser Thr Gln Val Pro Cys
 50 55 60
 Trp Leu Tyr Arg Ala Ile Leu Ser Leu Tyr Ile Leu Leu Ala Leu Ala
 65 70 75 80
 Phe Val Leu Cys Ile Ile Leu Ser Ala Phe Ile Met Val Lys Asn Ala
 85 90 95
 Glu Met Ser Lys Glu Leu Leu Gly Phe Lys Arg Glu Leu Trp Asn Val
 100 105 110
 Ser Asn Ser Val Gln Ala Cys Glu Glu Arg Gln Lys Arg Gly Trp Asp
 115 120 125
 Ser Val Gln Gln Ser Ile Thr Met Val Arg Ser Lys Ile Asp Arg Leu
 130 135 140
 Glu Thr Thr Leu Ala Gly Ile Lys Asn Ile Asp Thr Lys Val Gln Lys
 145 150 155 160
 Ile Leu Glu Val Leu Gln Lys Met Pro Gln Ser Ser Pro Gln

203/233

165

170

<210> 131

<211> 1908

<212> DNA

<213> Homo sapiens

<400> 131

atgaccacgt ggagcctccg gcggaggccg gcccgcacgc tgggactcct gctgctggtc	60
gtcttgggct tcctggtgct tcgcaggctg gactggagca ccctggtccc tctgcggctc	120
cgccatcgac agctggggct gcaggccaag ggctggaact tcatgctgga ggattccacc	180
ttctggatct tcgggggctc catccactat ttccgtgtgc ccagggaagta ctggagggac	240
cgcctgctga agatgaaggc ctgtggcttg aacacctca ccacctatgt tccgtggaac	300
ctgcatgagc cagaaagagg caaatgtgac ttctctggga acctggacct ggaggccttc	360
gtcctgatgg ccgcagagat cgggctgtgg gtgattctgc gtccaggccc ctacatctgc	420
agtgagatgg acctcggggg cttgcccagc tggctactcc aagacctgg catgaggctg	480
aggacaactt acaagggett caccgaagca gtggacctt attttgacca cctgatgtcc	540
aggggtggtg cactccagta caagcgtggg ggacctatca ttgccgtgca ggtggagaat	600
gaatatggtt cctataataa agaccccgca tacatgccct acgtcaagaa ggcactggag	660
gaccgtggca ttgtggaact gtcctgact tcagacaaca aggatgggct gagcaagggg	720
attgtccagg gagtcttggc caccatcaac ttgcagtcaa cacacgagct gcagctactg	780
accaccttcc tcttcaacgt ccaggggact cagcccaaga tggatgatgga gtactggacg	840
gggtggtttg actcgtgggg aggcctcac aatatcttgg attcttctga ggttttgaaa	900
accgtgtctg ccattgtgga cgcggctcc tccatcaacc tctacatgtt ccacggaggc	960
accaactttg gcttcatgaa tggagccatg cacttccatg actacaagtc agatgtcacc	1020
agctatgact atgatgctgt gotgacagaa gccggcgatt acacggccaa gtacatgaag	1080
cttcgagact tottggctc catctcaggc atccctctcc ctccccacc tgaccttctt	1140
cccaagatgc cgtatgagcc cttaacgcca gtcttgtacc tgtctctgtg ggacgcctc	1200
aagtacctgg gggagccaat caagtctgaa aagcccatca acatggagaa cctgccagtc	1260
aatgggggaa atggacagtc cttcgggtac attctctatg agaccagcat cacctcgtct	1320
ggcatcctca gtggccacgt gcatgatcg ggccaggtgt ttgtgaacac agtatccata	1380
ggattcttgg actacaagac aacgaagatt gctgtcccc tgatccaggg ttacaccgtg	1440
ctgaggatct tgggtggagaa tcgtgggcga gtcaactatg gggagaatat tgatgaccag	1500
cgcaaaggct taattggaaa tctctatctg aatgattcac ccctgaaaaa cttcagaatc	1560
tatagcctgg atatgaagaa gagcttctt cagaggttcg gcctggacaa atggagtcc	1620
ctcccagaaa caccacatt acctgcttcc ttcttgggta gcttgtccat cagctccacc	1680

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ccttgtgaca cctttctgaa gctggagggc tgggagaagg gggttgtatt catcaatggc 1740
 cagaaccttg gacgttactg gaacattgga cccagaaga cgctttacct cccagggtccc 1800
 tggttgagca gcggaatcaa ccagggtcat gtttttgagg agacgatggc gggccctgca 1860
 ttacagttca cggaaacccc ccacctgggc aggaaccagt acattaag 1908

<210> 132

<211> 954

<212> DNA

<213> Homo sapiens

<400> 132

atggttgagc tcatgttccc gctgttgctc ctccctctgc ccttccttct gtatatggct 60
 gcgccccaaa tcaggaaaat gctgtccagt ggggtgtgta catcaactgt tcagcttccct 120
 gggaaagtag ttgtggtcac aggagctaata acagggtatcg ggaaggagac agccaaagag 180
 ctggctcaga gaggagctcg agtatattta gcttgccggg atgtggaaaa gggggaattg 240
 gtggccaaag agatccagac cagcagaggg aaccagcagg tgttggtgag gaaactggac 300
 ctgtctgata ctaagtctat tcgagctttt gctaagggtt tcttagctga ggaaaagcac 360
 ctccacgttt tgatcaacaa tgcaggagtg atgatgtgtc cgtactcgaa gacagcagat 420
 ggctttgaga tgcacatagg agtcaaccac ttgggtcaact tcctcctaac ccatctgctg 480
 ctagagaaac taaaggaatc agcccatca aggatagtaa atgtgtcttc cctcgacat 540
 cacctgggaa ggatccactt ccataacctg cagggcgaga aattctacaa tgcaggcctg 600
 gcctactgtc acagcaagct agccaacatc ctcttcaccc aggaactggc ccggagacta 660
 aaaggctctg gcgttacgac gtattctgta caccctggca cagtccaatc tgaactgggt 720
 cggcactcat ctttcatgag atggatgtgg tggcttttct cctttttcat caagactcct 780
 cagcagggag cccagaccag cctgcaactgt gccttaacag aaggctttga gattctaagt 840
 gggaaatcatt tcagtgactg tcatgtggca tgggtctctg cccaagctcg taatgagact 900
 atagcaaggc ggctgtggga cgtcagttgt gacctgctgg gcctcccaat agac 954

<210> 133

<211> 246

<212> DNA

<213> Homo sapiens

<400> 133

atggccttta cctgtactc actgctgcag gcagccctgc totgcgtcaa cgccatcgca 60
 gtgctgcacg aggagcatt cctcaagaac attggctggg gaacagacca gggaaattgg 120
 ggatttgag aagagccggg aattaaatca cagctaataga acctattcg atctgtaaga 180

205/233

accgtgatga gagtgccatt gataatagta aactcaattg caattgtgtt acttttatta 240
 tttgga 246

<210> 134

<211> 741

<212> DNA

<213> Homo sapiens

<400> 134

atgcatcttg cacgtctggt cggtcctgc tccctccttc tgctactggg ggccctgtct 60
 ggatgggagg ccagcgatga cccattgag aaggtcattg aagggatcaa ccgagggctg 120
 agcaatgcag agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 180
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag ccacaccggc 240
 aaggagtgtg acaaaggcgt ccaggggctc aaccacggca tggacaaggt tgcccatgag 300
 atcaaccatg gtattggaca agcaggaaag gaagcagaga agcttgcca tggggtcaac 360
 aacgctgctg gacaggccgg gaaggaagca gacaaagcgg tccaagggtt ccacactggg 420
 gtccaccagg ctgggaagga agcagagaaa cttggccaag ggtcaacca tgctgctgac 480
 caggctggaa aggaagtga gaagcttggc caaggtgccc accatgctgc tggccaggcc 540
 gggaaggagc tgcagaatgc tcataatggg gtcaaccaag ccagcaagga ggccaaccag 600
 ctgctgaatg gcaaccatca aagcggtct tccagccatc aaggaggggc cacaaccacg 660
 ccgttagcct ctggggcctc ggtcaacacg cctttcatca accttcccgc cctgtggagg 720
 agcgtcgcca acatcatgcc c 741

<210> 135

<211> 618

<212> DNA

<213> Homo sapiens

<400> 135

atggccccc gccacctgc agtgcgggag atgaggggaag atgagaagcc cctgggtgctg 60
 gagatgctga aggccggcgt gaaggacacg gaaaaccgcg tggccctcca tgccttgaca 120
 cggccgcgg ccctgctcct cctggcggcg gccagcagcg gcctgcgctt tgcctggct 180
 tccttgcgcc tggccctcct cctgccggtg ttcttggtg tggccgcgt gaagctgggc 240
 ctgccccccc gatggggctc gctgcctccg ccgggtggcc tggggggccc ctgggtggcc 300
 gtgccccgct ccggtgacgt gtgtggggct ctggtctggt cccctggcac aaatgcaggg 360
 gacggggccc gggtcacccg cctgtctgtc tctcgtggc accgcgcgcg gggcgtgggc 420
 aggaggtgct tggccttcgc ggaggccccg gctcgggcct gggctggggg catgggggag 480

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ccccgggccc ggcctgtggt ccccggtggct gtggccgcct ggggggtggg agggatgctg	540
gagggtgtg gctaccaggc cgaggggggc tggggtgcc tgggtacac gctggtgagg	600
gaattcagca aagacctg	618

<210> 136

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 136

atggacgcca gatggtgggc agtgggtggtg ctggctgcgt tccccctccct aggggcagg	60
ggggagactc ccgaagcccc tccggagtea tggaccacgc tatggttctt ccgatttgtg	120
gtgaatgctg ctggctatgc cagctttatg gtacctggct acctcctggt gcagtacttc	180
aggcggaaga actacctgga gaccggtagg ggcctctgct tccccctggt gaaagcttgt	240
gtgttttgga atgagccaa ggcctctgat gaggttcccc tggcgccccg aacagaggcg	300
gcagagacca ccccgatgtg gcaggccctg aagctgctct tctgtgccac agggctccag	360
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acagccacat caccgggtga gcgctttacg gactgcagt tcttgggtgt aatgaaccga	480
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gcacccatgt accggtactc ctttgccagc ctgtccaatg tgcttagcag ctggtgccaa	600
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ctgacagcca cactcatctc cattgggggtc agcatgtttc tgctatccag cggaccagag	780
ccccgcagct cccagccac cacactctca ggcctcatct tactggcagg ttatatgtgt	840
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cagatgatgt ttgggggcaa tttcttctcc tgctcttca cagtgggtc actgctagaa	960
cagggggccc tactggaggg aaccgccttc atggggcgac acagtgagtt tgctgccc	1020
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cagtttgggg ctgccgtctt caccatcata atgacctcc gccaggcctt tgccatcctt	1140
ctttcctgcc ttctctatgg ccacactgtc actgtggtgg gagggctggg ggtggtgtg	1200
gtctttgtgt cctcctgtc cagagtctac gcgcggggcc gtctaaagca acggggaaa	1260
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<210> 137

<211> 918

<212> DNA

207/233

<213> Homo sapiens

<400> 137

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accccgagg	tgtgggttca	agttcggatg	gaggccaccg	agctctcgtc	cttcaccatc	120
cgttggtggg	tcctggggtc	tggctccatc	tccctgggtga	ctgtgagctg	ggggggcccc	180
gacggtgctg	gggggaccac	gctggctgtg	ttgcaccacg	aacgtggcat	ccggcaatgg	240
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tctggggcca	gcagccctg	cgccaacacc	acettctgct	gcaagtttgc	gtccttccct	360
gagggctcct	gggaggcctg	tgggagcctc	ccgcccagct	cagaccacag	gctctctgcc	420
ccgcgcactc	ctgcccccat	tctgcgggca	gacctggccg	ggatcttggg	ggtctcagga	480
gtcctcctct	ttggctgtgt	ctacctcctt	catctgctgc	gcgcacataa	gcaccgccct	540
gcccctaggg	tccagccgtc	ccgcaccagc	ccccaggcac	cgagagcacg	agcatgggca	600
ccaagccagg	cctcccaggc	tgctcttcac	gtcccttatg	ccactatcaa	caccagctgc	660
cgcgcagcta	ctttggacac	agctcaccac	catggggggc	cgtcctgggtg	ggcgtcactc	720
cccaccacag	ctgcacaccg	gccccagggc	cctgccgcct	gggcctccac	acccatccct	780
gcacgtggca	gctttgtctc	tgttgagaat	ggactctacg	ctcaggcagg	ggagaggcct	840
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<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

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agaaggggac	agcctcgtgt	ggtggtgatc	ggcgccggct	tggctggcct	ggctgcagcc	120
aaagcacttc	ttgagcagg	tttcacggat	gtcactgtgc	ttgaggcttc	cagccacatc	180
ggaggccgtg	tgagagtggt	gaaacttgga	cacgccacct	ttgagctggg	agccacctgg	240
atccatggct	cccatgggaa	ccctatctat	catctagcag	aagccaacgg	cctcctggaa	300
gagacaaccg	atgggggaacg	cagcgtgggc	cgcacacgcc	tctattccaa	gaatggcgtg	360
gcctgctacc	ttaccaacca	cggccgcagg	atccccaagg	acgtggttga	ggaattcagc	420
gatttataca	acgagggtcta	taacttgacc	caggagttct	tccggcacga	taaaccagtc	480
aatgctgaaa	gtcaaaatag	cgtgggggtg	ttcaccgcag	aggaggtgcg	taaccgcac	540
aggaatgacc	ctgacgaccc	agaggctacc	aagcgccctga	agctcgccat	gatccagcag	600
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gccttcgggg agtggaccga gatccccggc gctcaccaca tcatcccctc gggcttcatg	720
cgggttgtgg agctgctggc ggagggcacc cctgcccacg tcatccagct agggaaacct	780
gtccgctgca ttcactggga ccaggcctca gcccgcccca gaggccctga gattgagccc	840
cggggtgagg gcgaccacaa tcacgacact ggggaggggtg gccaggggtg agaggagccc	900
cgggggggca ggtgggatga ggatgagcag tggtcgggtg tggtgagtg cgaggactgt	960
gagctgatcc cggcggacca tgtgattgtg accgtgtcgc taggtgtgct aaagaggcag	1020
tacaccagtt tcttcgggcc aggcctgccc acagagaagg tggctgccat ccaccgcctg	1080
ggcattggca ccaccgacaa gatctttctg gaattcgagg agcccttctg gggccctgag	1140
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tctattcat acacgcaggt gggctccagc ggggaggatg tggagaaget ggccaagccc	1500
ctgccgtaca cggagagctc aaagacagcg cccatgcagg tgetgttttc cggtgaggcc	1560
accaccgca agtactattc caccaccac ggtgctctgc tgtccggcca gcgtgaggct	1620
gcccgctca ttgagatgta ccgagacctc ttccagcagg ggacc	1665

<210> 139

<211> 750

<212> DNA

<213> Homo sapiens

<400> 139

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gtggaattca ccgggagaga tagcatcacc tgtctcacgt gccaggggac aggctacatt	180
ccaacagagc aagtaaata gttgggtggc ttgatcccac acagtgatca gagattgcgc	240
cctcagcgaa ctaagcaata tgtcctcctg tccatcctgc tttgtctcct ggcattctgg	300
ttggtggttt tcttcctggt tccgcattca gtccttgttg atgatgacgg catcaaagt	360
gtgaaagtca catttaataa gcaagactcc cttgtaattc tcaccatcat ggccaccctg	420
aaaatcagga actccaactt ctacacggtg gcagtgaaca gcctgtccag ccagattcag	480
tacatgaaca cagtggtcag tacatatgtg actactaacg tctcccttat tccacctcgg	540
agtgaacaac tggatgaattt tacggggaag gccgagatgg gaggaccgtt ttctatgtg	600
tactttctct gcacgggtacc tgagatcctg gtgcacaaca tagtgatctt catgcgaact	660
tcagtgaaga ttcatatcat tggcctcatg acccagagct ccttgagagac acatcactat	720

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gtggattgtg gaggaattc cacagctatt

750

<210> 140

<211> 522

<212> DNA

<213> Homo sapiens

<400> 140

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catgacccag actatgagaa tatcaccttg gccttcaaaa atcaggacca tgcaaaggggt	120
ggtcattcac gaccacgag ccaagtccca gccagtgca ggccgccctc agactccacc	180
caggtccccct gctggttgta cagagccatc ctgagcctgt acatcctcct ggccctggcc	240
tttgtcctct gcatcatcct gtcagccttc atcatggtga agaatgctga gatgtccaag	300
gagctgctgg gctttaaaag ggagctttgg aatgtotcaa actccgtaca agcatgcgaa	360
gagagacaga agagaggctg ggattccgtt cagcagagca tcaccatggt caggagcaag	420
attgatagat tagagacgac attagcaggc ataaaaaaca ttgacacaaa ggtacagaaa	480
atcttgaggg tgctgcagaa aatgccacag tcctcacctc aa	522

<210> 141

<211> 3234

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)...(2039)

<400> 141

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aggctcccgc gcgcggctga gtgoggactg gagtgggaac ccgggtcccc gcgcttagag	120
aacacgcy atg acc acg tgg agc ctc cgg cgg agg ccg gcc cgc acg ctg	170
Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu	
1 5 10	
gga ctc ctg ctg ctg gtc gtc ttg ggc ttc ctg gtg ctt cgc agg ctg	218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu	
15 20 25 30	
gac tgg agc acc ctg gtc cct ctg cgg ctc cgc cat cga cag ctg ggg	266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly	

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35	40	45	
ctg cag gcc aag ggc tgg aac ttc atg ctg gag gat tcc acc ttc tgg			314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp			
50	55	60	
atc ttc ggg ggc tcc atc cac tat ttc cgt gtg ccc agg gag tac tgg			362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp			
65	70	75	
agg gac cgc ctg ctg aag atg aag gcc tgt ggc ttg aac acc ctc acc			410
Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr			
80	85	90	
acc tat gtt ccg tgg aac ctg cat gag cca gaa aga ggc aaa ttt gac			458
Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp			
95	100	105	110
ttc tct ggg aac ctg gac ctg gag gcc ttc gtc ctg atg gcc gca gag			506
Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu			
115	120	125	
atc ggg ctg tgg gtg att ctg cgt cca ggc ccc tac atc tgc agt gag			554
Ile Gly Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu			
130	135	140	
atg gac ctc ggg ggc ttg ccc agc tgg cta ctc caa gac cct ggc atg			602
Met Asp Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met			
145	150	155	
agg ctg agg aca act tac aag ggc ttc acc gaa gca gtg gac ctt tat			650
Arg Leu Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr			
160	165	170	
ttt gac cac ctg atg tcc agg gtg gtg cca ctc cag tac aag cgt ggg			698
Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly			
175	180	185	190
gga cct atc att gcc gtg cag gtg gag aat gaa tat ggt tcc tat aat			746
Gly Pro Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn			
195	200	205	
aaa gac ccc gca tac atg ccc tac gtc aag aag gca ctg gag gac cgt			794
Lys Asp Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg			
210	215	220	
ggc att gtg gaa ctg ctc ctg act tca gac aac aag gat ggg ctg agc			842

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Gly Ile Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser	
225 230 235	
aag ggg att gtc cag gga gtc ttg gcc acc atc aac ttg cag tca aca	890
Lys Gly Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr	
240 245 250	
cac gag ctg cag cta ctg acc acc ttt ctc ttc aac gtc cag ggg act	938
His Glu Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr	
255 260 265 270	
cag ccc aag atg gtg atg gag tac tgg acg ggg tgg ttt gac tgg tgg	986
Gln Pro Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp	
275 280 285	
gga ggc cct cac aat atc ttg gat tct tct gag gtt ttg aaa acc gtg	1034
Gly Gly Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val	
290 295 300	
tct gcc att gtg gac gcc ggc tcc tcc atc aac ctc tac atg ttc cac	1082
Ser Ala Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His	
305 310 315	
gga ggc acc aac ttt ggc ttc atg aat gga gcc atg cac ttc cat gac	1130
Gly Gly Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp	
320 325 330	
tac aag tca gat gtc acc agc tat gac tat gat gct gtg ctg aca gaa	1178
Tyr Lys Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu	
335 340 345 350	
gcc ggc gat tac acg gcc aag tac atg aag ctt cga gac ttc ttc ggc	1226
Ala Gly Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly	
355 360 365	
tcc atc tca ggc atc cct ctc cct ccc cca cct gac ctt ctt ccc aag	1274
Ser Ile Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys	
370 375 380	
atg ccg tat gag ccc tta acg cca gtc ttg tac ctg tct ctg tgg gac	1322
Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp	
385 390 395	
gcc ctc aag tac ctg ggg gag cca atc aag tct gaa aag ccc atc aac	1370
Ala Leu Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn	
400 405 410	

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atg gag aac ctg cca gtc aat ggg gga aat gga cag tcc ttc ggg tac	1418
Met Glu Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr	
415 420 425 430	
att ctc tat gag acc agc atc acc tcg tct ggc atc ctc agt ggc cac	1466
Ile Leu Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His	
435 440 445	
gtg cat gat cgg ggg cag gtg ttt gtg aac aca gta tcc ata gga ttc	1514
Val His Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe	
450 455 460	
ttg gac tac aag aca acg aag att gct gtc ccc ctg atc cag ggt tac	1562
Leu Asp Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr	
465 470 475	
acc gtg ctg agg atc ttg gtg gag aat cgt ggg cga gtc aac tat ggg	1610
Thr Val Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly	
480 485 490	
gag aat att gat gac cag cgc aaa ggc tta att gga aat ctc tat ctg	1658
Glu Asn Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu	
495 500 505 510	
aat gat tca ccc ctg aaa aac ttc aga atc tat agc ctg gat atg aag	1706
Asn Asp Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys	
515 520 525	
aag agc ttc ttt cag agg ttc ggc ctg gac aaa tgg agt tcc ctc cca	1754
Lys Ser Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro	
530 535 540	
gaa aca ccc aca tta cct gct ttc ttc ttg ggt agc ttg tcc atc agc	1802
Glu Thr Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser	
545 550 555	
tcc acc cct tgt gac acc ttt ctg aag ctg gag ggc tgg gag aag ggg	1850
Ser Thr Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly	
560 565 570	
gtt gta ttc atc aat ggc cag aac ctt gga cgt tac tgg aac att gga	1898
Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly	
575 580 585 590	
ccc cag aag acg ctt tac ctc cca ggt ccc tgg ttg agc agc gga atc	1946
Pro Gln Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile	

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595	600	605	
aac cag gtc atc gtt ttt gag gag acg atg gcg ggc cct gca tta cag			1994
Asn Gln Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln			
610	615	620	
ttc acg gaa acc ccc cac ctg ggc agg aac cag tac att aag tgag			2040
Phe Thr Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys			
625	630	635	
cggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc			2100
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg			2160
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg			2220
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cagaaaaagt gctgaaacgt gcccttgca cggacgtcac agccctgcga gcatctgctg			2400
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tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc			2520
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agccatggcc catgtctgca catccaggga ggaggacaga agggccagct cacatgtgag			2940
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga agggccagct			3000
cacatgtgag tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga			3060
agggccagct cagtggcccc cgccccccac cccccacgcc cgaacagcag gggcagagca			3120
gcctccttc gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac			3180
acctggcttg ggctcaactgt cctgagttgc agtaaagcta taacctgaa tcac			3234

<210> 142

<211> 2490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)...(1026)

214/233

<400> 142

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      Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro
              1              5              10
ttc ctt ctg tat atg gct gcg ccc caa atc agg aaa atg ctg tcc agt      159
Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser
      15              20              25              30
ggg gtg tgt aca tca act gtt cag ctt cct ggg aaa gta gtt gtg gtc      207
Gly Val Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val
              35              40              45
aca gga gct aat aca ggt atc ggg aag gag aca gcc aaa gag ctg gct      255
Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala
              50              55              60
cag aga gga gct cga gta tat tta gct tgc cgg gat gtg gaa aag ggg      303
Gln Arg Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly
              65              70              75
gaa ttg gtg gcc aaa gag atc cag acc acg aca ggg aac cag cag gtg      351
Glu Leu Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val
              80              85              90
ttg gtg cgg aaa ctg gac ctg tct gat act aag tct att cga gct ttt      399
Leu Val Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe
      95              100              105              110
gct aag ggc ttc tta gct gag gaa aag cac ctc cac gtt ttg atc aac      447
Ala Lys Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn
              115              120              125
aat gca gga gtg atg atg tgt ccg tac tcg aag aca gca gat ggc ttt      495
Asn Ala Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe
              130              135              140
gag atg cac ata gga gtc aac cac ttg ggt cac ttc ctc cta acc cat      543
Glu Met His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His
              145              150              155
ctg ctg cta gag aaa cta aag gaa tca gcc cca tca agg ata gta aat      591
Leu Leu Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn
              160              165              170

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gtg tct tcc ctc gca cat cac ctg gga agg atc cac ttc cat aac ctg	639
Val Ser Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu	
175 180 185 190	
cag ggc gag aaa ttc tac aat gca ggc ctg gcc tac tgt cac agc aag	687
Gln Gly Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys	
195 200 205	
cta gcc aac atc ctc ttc acc cag gaa ctg gcc cgg aga cta aaa ggc	735
Leu Ala Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly	
210 215 220	
tct ggc gtt acg acg tat tct gta cac cct ggc aca gtc caa tct gaa	783
Ser Gly Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu	
225 230 235	
ctg gtt cgg cac tca tct ttc atg aga tgg atg tgg tgg ctt ttc tcc	831
Leu Val Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser	
240 245 250	
ttt ttc atc aag act cct cag cag gga gcc cag acc agc ctg cac tgt	879
Phe Phe Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys	
255 260 265 270	
gcc tta aca gaa ggt ctt gag att cta agt ggg aat cat ttc agt gac	927
Ala Leu Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp	
275 280 285	
tgt cat gtg gca tgg gtc tct gcc caa gct cgt aat gag act ata gca	975
Cys His Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala	
290 295 300	
agg cgg ctg tgg gac gtc agt tgt gac ctg ctg ggc ctc cca ata gac	1023
Arg Arg Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp	
305 310 315	
taacagg cagtgccagt tggacccaag agaagactgc agcagactac acagtacttc	1080
ttgtcaaaat gatttcctt caaggttttc aaaaccttta gcacaaagag agcaaaacct	1140
tccagccttg cctgcttggt gtccagttaa aactcagtgt actgccagat tcgtctaaat	1200
gtctgtcatg tccagattta ctttgccttct gttactgcca gagttactag agatatcata	1260
ataggataag aagacctca tatgacctgc acagctcatt ttccttctga aagaaaactac	1320
tacctaggag aatotaagct atagcaggga tgatttatgc aaatttgaac tagcttcttt	1380
gttcacaatt cagttcctcc caaccaacca gtcttcactt caagagggcc acactgcaac	1440
ctcagcttaa catgaataac aaagactggc tcaggagcag ggcttgccca ggcattggtgg	1500

216/233

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atcacccggag gtcagtagtt caagaccagc ctggccaaca tggatgaaacc ccacctctac 1560
taaaaattgt gtatatcttt gtgtgtcttc ctgtttatgt gtgccaaggg agtattttca 1620
caaagttcaa aacagccaca ataatcagag atggagcaaa ccagtgccat ccagtcttta 1680
tgcaaatgaa atgctgcaaa gggaagcaga ttctgtatat gttggtaact acccaccaag 1740
agcacatggg tagcagggaa gaagtaaaaa aagagaagga gaatactgga agataatgca 1800
caaaatgaag ggactagtta aggattaact agccctttta ggattaacta gttaaggatt 1860
aatagcaaaa gatattaaat atgctaacat agctatggag gaattgaggg caagcaccca 1920
ggactgatga ggtcttaaca aaaaccagtg tggcaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaaaaatcc taaaaacaaa caaacaaaaa aaacaattct tcattcagaa aaattatctt 2040
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gtcttgacaa gattaaaatg tctgtgccaa aattttgtat tttatttgga gacttcttat 2160
caaaagtaat gctgccaaag gaagtctaag gaattagtag tgttcccatc acttgtttg 2220
agtgtgctat tctaaaagat tttgatttcc tggaatgaca attatatttt aactttggtg 2280
ggggaaagag ttataggacc acagtcttca cttctgatac ttgtaaatta atcttttatt 2340
gcacttgttt tgaccattaa gctatatgtt tagaaatggt cattttacgg aaaaattaga 2400
aaaattctga taatagtga gaataaatga attaattgtt tacttaattt atattgaact 2460
gtcaatgaca aataaaaatt ctttttgatt 2490

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<210> 143

<211> 1465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)...(332)

<400> 143

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Met Ala Phe Thr Leu Tyr Ser Leu Leu
1 5
cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag gag 158
Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu Glu
10 15 20 25
cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt gga 206
Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly Gly

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30	35	40	
ttt gga gaa gag ccg gga att aaa tca cag cta atg aac ctt att cga			254
Phe Gly Glu Glu Pro Gly Ile Lys Ser Gln Leu Met Asn Leu Ile Arg			
45	50	55	
tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca att			302
Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser Ile			
60	65	70	
gca att gtg tta ctt tta tta ttt gga tgaatatcag tggagaaaat g			350
Ala Ile Val Leu Leu Leu Leu Phe Gly			
75	80		
gagactcaga agaggacatg ccagtagaag ttattacttt ggtcattatt ggaatattta			410
tatotttagct ggctgacctt gcacttgtaaaa gctgaaaata aaaccagggt			470
ttotatttat ctgttttttt ttttaagtgt gcacttgtag tttcattaca aaagatcaga			530
tcataaaagg cagtaactct ccaggactgg aatatctgat tgcctcagtg taatagtagt			590
tcatactgtg gtgagattgt taaaagggtg caagactgtt gcttctcttt ttttagatat			650
ttttctatct ctcaactctc agggatgaaa ttctttttca aagttttgaa gttccttgca			710
acttagccat gatgtgagtg gttatcccta gataaaaatta aaaggatttt taaaaagtaa			770
ttactgcaca taaaatgata aataggtaat ttgaataatt ttattttaag ctcttggtt			830
aattattttg tctattgtct cagctataaa ttcaaattta tacatactat tgagtattaa			890
tattctctga tttcaggagg aattctgtca gtcacatgat gattatgttt ttgtttaaca			950
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tatttcttgg tggagcagca cattgtggag tgtgattctt aattcttcat tgagtttgc			1250
aataggacat tgatgctgga taggttgtct tttgttttta tgtctcagac catcttgtga			1310
gattgtttgc ctatctcata atacagtttt atgcagaaag gttgaaacta tgtaaatggt			1370
ttttatggaa attatcagtt acaatatttt aaagggtgtag aatggcatct ttgtttatag			1430
gagaacattt gtaaataaag ttaaatttct aagtc			1465

<210> 144

<211> 917

<212> DNA

<213> Homo sapiens

<220>

218/233

<221> CDS

<222> (32)...(775)

<400> 144

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Met His Leu Ala Arg Leu Val				
1 5				
ggc tcc tgc tcc ctc ctt ctg cta ctg ggg gcc ctg tct gga tgg gcg	100			
Gly Ser Cys Ser Leu Leu Leu Leu Leu Gly Ala Leu Ser Gly Trp Ala				
10 15 20				
gcc agc gat gac ccc att gag aag gtc att gaa ggg atc aac cga ggg	148			
Ala Ser Asp Asp Pro Ile Glu Lys Val Ile Glu Gly Ile Asn Arg Gly				
25 30 35				
ctg agc aat gca gag aga gag gtg ggc aag gcc ctg gat ggc atc aac	196			
Leu Ser Asn Ala Glu Arg Glu Val Gly Lys Ala Leu Asp Gly Ile Asn				
40 45 50 55				
agt gga atc acg cat gcc gga agg gaa gtg gag aag gtt ttc aac gga	244			
Ser Gly Ile Thr His Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly				
60 65 70				
ctt agc aac atg ggg agc cac acc ggc aag gag ttg gac aaa ggc gtc	292			
Leu Ser Asn Met Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val				
75 80 85				
cag ggg ctc aac cac ggc atg gac aag gtt gcc cat gag atc aac cat	340			
Gln Gly Leu Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His				
90 95 100				
ggt att gga caa gca gga aag gaa gca gag aag ctt ggc cat ggg gtc	388			
Gly Ile Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val				
105 110 115				
aac aac gct gct gga cag gcc ggg aag gaa gca gac aaa gcg gtc caa	436			
Asn Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln				
120 125 130 135				
ggg ttc cac act ggg gtc cac cag gct ggg aag gaa gca gag aaa ctt	484			
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu				
140 145 150				
ggc caa ggg gtc aac cat gct gct gac cag gct gga aag gaa gtg gag	532			
Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu				

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155	160	165	
aag ctt ggc caa ggt gcc cac cat gct gct ggc cag gcc ggg aag gag			580
Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Lys Glu			
170	175	180	
ctg cag aat gct cat aat ggg gtc aac caa gcc agc aag gag gcc aac			628
Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser Lys Glu Ala Asn			
185	190	195	
cag ctg ctg aat ggc aac cat caa agc gga tct tcc agc cat caa gga			676
Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser Ser Ser His Gln Gly			
200	205	210	215
ggg gcc aca acc acg ccg tta gcc tct ggg gcc tcg gtc aac acg cct			724
Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly Ala Ser Val Asn Thr Pro			
220	225	230	
ttc atc aac ctt ccc gcc ctg tgg agg agc gtc gcc aac atc atg ccc			772
Phe Ile Asn Leu Pro Ala Leu Trp Arg Ser Val Ala Asn Ile Met Pro			
235	240	245	
taaactgg catccggcct tgctgggaga ataatgtcgc cgttgtcaca tcagctgaca			830
tgacctggag ggggtggggg tgggggacag gtttctgaaa tccctgaagg gggttgtact			890
gggatttgtg aataaacttg atacact			917

<210> 145

<211> 1306

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)...(694)

<400> 145

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cctggggggt gcc atg gcc ccc agc cac ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc ggc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	

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gac acg gaa aac cgc gtg gcc ctc cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctc ctc ctg gcg gcg gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctc ctc ctg ccg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg cgg gcc cga tgg ggc tcg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggg ggc ccc tgg gtg gcc gtg cgg ggc tcc ggt gac gtg tgt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	
95 100 105	
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg	445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg	
110 115 120	
gtc acc cgc ctg tct gtc tct cgc tgg cac cgc cgc cgg ggc gtg ggc	493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly	
125 130 135 140	
agg agg ctg ctg gcc ttc gcg gag gcc cgg gct cgg gcc tgg gct ggg	541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly	
145 150 155	
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc	589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala	
160 165 170	
gcc tgg ggg gtg gga ggg atg ctg gag ggc tgt ggc tac cag gcc gag	637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu	
175 180 185	
ggg ggc tgg ggc tgc ctg ggc tac acg ctg gtg agg gaa ttc agc aaa	685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys	
190 195 200	
gac ctg tgaagctaca gactgacagc cagggcaggg gaggagggag gggcgccag	740
Asp Leu	

221/233

205

cacctgatga tcgcctactg tctgcgggtt cttttacctg ctctccctca gtgagtcctc	800
aaccaccctg ggcccagaaa cagaggcctg ccgaggggag gagcctggcc tctgtccacc	860
cgtcagcagt gtgaagtctg ttgtgtttga gcttctcaga gtggaatgac tccttttct	920
tcctggccct cgggggacctc tcgaggtcag cctctccaac ccctacctca gctcctgtct	980
gcaactgagaa acctccccgg gtgatgtctg caaagtctgt gctgtccgtg ccccaggctg	1040
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tgcgactccg cctccctggg acctggattg ggtcagatgc ctgtccttgg aggggacaag	1160
gttgactgct taggaggcgc gacgcacagg gctgccagge ctggcccctc tctgggaagg	1220
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tttgtaata aagcctgaaa ccgctt	1306

<210> 146

<211> 2022

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)...(1416)

<400> 146

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gcgcggcccc gggactcgca ttccccggtt cccctccac cccacgcggc ctggacc	117
atg gac gcc aga tgg tgg gca gtg gtg ctg gct gcg ttc ccc tcc	165
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser	
1 5 10 15	
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc	213
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr	
20 25 30	
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc	261
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser	
35 40 45	
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac	309
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn	
50 55 60	
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt	357

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Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys		
65					70					75					80		
gtg	ttt	ggc	aat	gag	ccc	aag	gcc	tct	gat	gag	gtt	ccc	ctg	gcg	ccc	405	
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro		
			85						90						95		
cga	aca	gag	gcg	gca	gag	acc	acc	cgc	atg	tgg	cag	gcc	ctg	aag	ctg	453	
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu		
			100						105						110		
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	501	
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val		
			115						120						125		
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	549	
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser		
			130						135						140		
cgc	ggt	gag	cgc	ttt	acg	gac	tcg	cag	ttc	ctg	gtg	cta	atg	aac	cga	597	
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg		
			145						150						155		
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	gtt	ctc	tgc	aag	cag	645	
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln		
			165						170						175		
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	693	
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser		
			180						185						190		
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	741	
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser		
			195						200						205		
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	789	
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met		
			210						215						220		
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	837	
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr		
			225						230						235		
ctg	aca	gcc	aca	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	885	
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser		
			245						250						255		

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agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc etc	933
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	981
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt	1029
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1077
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1125
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1173
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1221
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	
355 360 365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt	1269
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	
370 375 380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg	1317
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	
385 390 395 400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag	1365
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys	
405 410 415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt	1413
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val	
420 425 430	
tgagggt ggaaagggcc tgagggtga agtgaaatag gaccctccca ccatccccctt	1470
ctgctgtaac ctctgagga gctggctgaa agggcaaat gcaggtgttt totcagtatc	1530

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acagaccagc tctgcagcag gggattgggg agcccaggag gcagcettcc cttttgcett 1590
aagtcaccca tcttccagta agcagtttat tctgagcccc gggggtagac agtcctcagt 1650
gagggggtttt ggggagtttg ggggtcaagag agcataggta ggttccacag ttactcttcc 1710
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ctgcaaatac ctgcattttct taccctgggtg agaaaagcac aagcgggtgta ggetccaatg 1830
ctgctttccc aggaggggtga agatgggtgct gtgctgagga aaggggatgc agagccctgc 1890
ccagcaccac cacctcctat gctcctggat ccctaggtct tgttccatga gcctgttgca 1950
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ttactgcagt gg 2022

<210> 147

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(995)

<400> 147

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gactgtaggg ggcc atg ggg cac cgg acc ctg gtc ctg ccc tgg gtg ctg 110
Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu
1 5 10
ctg acc ttg tgt gtc act gcg ggg acc ccg gag gtg tgg gtt caa gtt 158
Leu Thr Leu Cys Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val
15 20 25
cgg atg gag gcc acc gag ctg tgc tcc ttc acc atc cgt tgt ggg ttc 206
Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe
30 35 40
ctg ggg tct ggc tcc atc tcc ctg gtg act gtg agc tgg ggg ggc ccc 254
Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro
45 50 55 60
gac ggt gct ggg ggg acc acg ctg gct gtg ttg cac cca gaa cgt ggc 302
Asp Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly
65 70 75
atc cgg caa tgg gcc cct gct cgc cag gcc cgc tgg gaa acc cag agc 350

225/233

Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser	
80 85 90	
agc atc tct ctc atc ctg gaa ggc tct ggg gcc agc agc ccc tgc gcc	398
Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala	
95 100 105	
aac acc acc ttc tgc tgc aag ttt gcg tcc ttc cct gag ggc tcc tgg	446
Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp	
110 115 120	
gag gcc tgt ggg agc ctc ccg ccc agc tca gac cca ggg ctc tct gcc	494
Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala	
125 130 135 140	
ccg ccg act cct gcc ccc att ctg cgg gca gac ctg gcc ggg atc ttg	542
Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu	
145 150 155	
ggg gtc tca gga gtc ctc ctc ttt ggc tgt gtc tac ctc ctt cat ctg	590
Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu	
160 165 170	
ctg cgc cga cat aag cac cgc cct gcc cct agg ctc cag ccg tcc cgc	638
Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg	
175 180 185	
acc agc ccc cag gca ccg aga gca cga gca tgg gca cca agc cag gcc	686
Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala	
190 195 200	
tcc cag gct gct ctt cac gtc cct tat gcc act atc aac acc agc tgc	734
Ser Gln Ala Ala Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys	
205 210 215 220	
cgc cca gct act ttg gac aca gct cac ccc cat ggg ggg ccg tcc tgg	782
Arg Pro Ala Thr Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp	
225 230 235	
tgg gcg tca ctc ccc acc cac gct gca cac cgg ccc cag ggc cct gcc	830
Trp Ala Ser Leu Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala	
240 245 250	
gcc tgg gcc tcc aca ccc atc cct gca cgt ggc agc ttt gtc tct gtt	878
Ala Trp Ala Ser Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val	
255 260 265	

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gag aat gga ctc tac gct cag gca ggg gag agg cct cct cac act ggt 926
 Glu Asn Gly Leu Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly
 270 275 280
 ccc ggc ctc act ctt ttc cct gac cct cgg ggg ccc agg gcc atg gaa 974
 Pro Gly Leu Thr Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu
 285 290 295 300
 gga ccc tta gga gtt cga tgagagagac catgaggcca ctgggctt 1020
 Gly Pro Leu Gly Val Arg
 305
 tccccctccc aggcctcctg ggtgtcaccc ccttacttta attcttgggc ctccaataag 1080
 tgteccatag gtgtctggcc aggccacct gctgaggatg tggctctgtg gcgtgtgtgg 1140
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 agtcagcaac acagttttctc tgatgtc 1227

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 ggccgagacc ggagcgccgc tcgccgcaga cttacttccc cggctcagca gggaaaggtt 180
 cctagaaggt gagcgcggaac ggt atg caa agt tgt gaa tcc agt ggt gac agt 233
 Met Gln Ser Cys Glu Ser Ser Gly Asp Ser
 1 5 10
 gcg gat gac cct ctc agt cgc ggc cta cgg aga agg gga cag cct cgt 281
 Ala Asp Asp Pro Leu Ser Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg
 15 20 25
 gtg gtg gtg atc ggc gcc ggc ttg gct ggc ctg gct gca gcc aaa gca 329
 Val Val Val Ile Gly Ala Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala
 30 35 40
 ctt ctt gag cag ggt ttc acg gat gtc act gtg ctt gag gct tcc agc 377

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Leu Leu Glu Gln Gly Phe Thr Asp Val Thr Val Leu Glu Ala Ser Ser	
45 50 55	
cac atc gga ggc cgt gtg cag agt gtg aaa ctt gga cac gcc acc ttt	425
His Ile Gly Gly Arg Val Gln Ser Val Lys Leu Gly His Ala Thr Phe	
60 65 70	
gag ctg gga gcc acc tgg atc cat ggc tcc cat ggg aac cct atc tat	473
Glu Leu Gly Ala Thr Trp Ile His Gly Ser His Gly Asn Pro Ile Tyr	
75 80 85 90	
cat cta gca gaa gcc aac ggc ctc ctg gaa gag aca acc gat ggg gaa	521
His Leu Ala Glu Ala Asn Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu	
95 100 105	
cgc agc gtg ggc cgc atc agc ctc tat tcc aag aat ggc gtg gcc tgc	569
Arg Ser Val Gly Arg Ile Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys	
110 115 120	
tac ctt acc aac cac ggc cgc agg atc ccc aag gac gtg gtt gag gaa	617
Tyr Leu Thr Asn His Gly Arg Arg Ile Pro Lys Asp Val Val Glu Glu	
125 130 135	
ttc agc gat tta tac aac gag gtc tat aac ttg acc cag gag ttc ttc	665
Phe Ser Asp Leu Tyr Asn Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe	
140 145 150	
cgg cac gat aaa cca gtc aat gct gaa agt caa aat agc gtg ggg gtg	713
Arg His Asp Lys Pro Val Asn Ala Glu Ser Gln Asn Ser Val Gly Val	
155 160 165 170	
ttc acc cga gag gag gtg cgt aac cgc atc agg aat gac cct gac gac	761
Phe Thr Arg Glu Glu Val Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp	
175 180 185	
cca gag gct acc aag cgc ctg aag ctc gcc atg atc cag cag tac ctg	809
Pro Glu Ala Thr Lys Arg Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu	
190 195 200	
aag gtg gag agc tgt gag agc agc tca cac agc atg gac gag gtg tcc	857
Lys Val Glu Ser Cys Glu Ser Ser Ser His Ser Met Asp Glu Val Ser	
205 210 215	
ctg agc gcc ttc ggg gag tgg acc gag atc ccc ggc gct cac cac atc	905
Leu Ser Ala Phe Gly Glu Trp Thr Glu Ile Pro Gly Ala His His Ile	
220 225 230	

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atc ccc tcg ggc ttc atg cgg gtt gtg gag ctg ctg gcg gag ggc atc	953
Ile Pro Ser Gly Phe Met Arg Val Val Glu Leu Leu Ala Glu Gly Ile	
235 240 245 250	
cct gcc cac gtc atc cag cta ggg aaa cct gtc cgc tgc att cac tgg	1001
Pro Ala His Val Ile Gln Leu Gly Lys Pro Val Arg Cys Ile His Trp	
255 260 265	
gac cag gcc tca gcc cgc ccc aga ggc cct gag att gag ccc cgg ggt	1049
Asp Gln Ala Ser Ala Arg Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly	
270 275 280	
gag ggc gac cac aat cac gac act ggg gag ggt ggc cag ggt gga gag	1097
Glu Gly Asp His Asn His Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu	
285 290 295	
gag ccc cgg ggg ggc agg tgg gat gag gat gag cag tgg tcg gtg gtg	1145
Glu Pro Arg Gly Gly Arg Trp Asp Glu Asp Glu Gln Trp Ser Val Val	
300 305 310	
gtg gag tgc gag gac tgt gag ctg atc ccg gcg gac cat gtg att gtg	1193
Val Glu Cys Glu Asp Cys Glu Leu Ile Pro Ala Asp His Val Ile Val	
315 320 325 330	
acc gtg tcg cta ggt gtg cta aag agg cag tac acc agt ttc ttc cgg	1241
Thr Val Ser Leu Gly Val Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg	
335 340 345	
cca ggc ctg ccc aca gag aag gtg gct gcc atc cac cgc ctg ggc att	1289
Pro Gly Leu Pro Thr Glu Lys Val Ala Ala Ile His Arg Leu Gly Ile	
350 355 360	
ggc acc acc gac aag atc ttt ctg gaa ttc gag gag ccc ttc tgg ggc	1337
Gly Thr Thr Asp Lys Ile Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly	
365 370 375	
cct gag tgc aac agc cta cag ttt gtg tgg gag gac gaa gcg gag agc	1385
Pro Glu Cys Asn Ser Leu Gln Phe Val Trp Glu Asp Glu Ala Glu Ser	
380 385 390	
cac acc ctc acc tac cca cct gag ctc tgg tac cgc aag atc tgc ggc	1433
His Thr Leu Thr Tyr Pro Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly	
395 400 405 410	
ttt gat gtc ctc tac ccg cct gag cgc tac ggc cat gtg ctg agc ggc	1481
Phe Asp Val Leu Tyr Pro Pro Glu Arg Tyr Gly His Val Leu Ser Gly	

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415	420	425	
tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag			1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu			
430	435	440	
gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac			1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn			
445	450	455	
ccc aac att cca aaa cct cgg cga atc ttg cgc tcg gcc tgg ggc agc			1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser			
460	465	470	
aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc			1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser			
475	480	485	490
ggg gcg gat gtg gag aag ctg gcc aag ccc ctg ccg tac acg gag agc			1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser			
495	500	505	
tca aag aca gcg ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac			1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His			
510	515	520	
cgc aag tac tat tcc acc acc cac ggt gct ctg ctg tcc ggc cag cgt			1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg			
525	530	535	
gag gct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg			1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly			
540	545	550	
acc tgagggctgt cctcgctgtt gagaagagcc actaactcgt gacctccagc ct			1920
Thr			
555			
gccccttget gccgtgtget cctgccttcc tgatcctctg tagaaaggat ttttatcttc			1980
tgtagagcta gccgccctga ctgccttcag acctggccct gtagcttttc tttttctcca			2040
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ttgcctaccc tctgtcctgc cttgttattg taagtgcctt caatactttg cattttggga			2160
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230/233

<211> 1493

<212> DNA

<213> Homo sapiens

<220>

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<222> (93)...(845)

<400> 149

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gcaggacatg acaccagtgg catatcacgg cc atg ggg tct cag cat tcc gct      113
                               Met Gly Ser Gln His Ser Ala
                               1             5

gct gct cgc ccc tcc tcc tgc agg cga aag caa gaa gat gac agg gac      161
Ala Ala Arg Pro Ser Ser Cys Arg Arg Lys Gln Glu Asp Asp Arg Asp
      10             15             20

ggg ttg ctg gct gaa cga gag cag gaa gaa gcc att gct cag ttc cca      209
Gly Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro
      25             30             35

tat gtg gaa ttc acc ggg aga gat agc atc acc tgt ctc acg tgc cag      257
Tyr Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys Gln
      40             45             50             55

ggg aca ggc tac att cca aca gag caa gta aat gag ttg gtg gct ttg      305
Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala Leu
      60             65             70

atc cca cac agt gat cag aga ttg cgc cct cag cga act aag caa tat      353
Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln Tyr
      75             80             85

gtc ctc ctg tcc atc ctg ctt tgt ctc ctg gca tct ggt ttg gtg gtt      401
Val Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val
      90             95             100

ttc ttc ctg ttt ccg cat tca gtc ctt gtg gat gat gac ggc atc aaa      449
Phe Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys
      105             110             115

gtg gtg aaa gtc aca ttt aat aag caa gac tcc ctt gta att ctc acc      497
Val Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr
      120             125             130             135

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atc atg gcc acc ctg aaa atc agg aac tcc aac ttc tac acg gtg gca	545
Ile Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala	
140 145 150	
gtg acc agc ctg tcc agc cag att cag tac atg aac aca gtg gtc agt	593
Val Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Ser	
155 160 165	
aca tat gtg act act aac gtc tcc ctt att cca cct cgg agt gag caa	641
Thr Tyr Val Thr Thr Asn Val Ser Leu Ile Pro Pro Arg Ser Glu Gln	
170 175 180	
ctg gtg aat ttt acc ggg aag gcc gag atg gga gga ccg ttt tcc tat	689
Leu Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr	
185 190 195	
gtg tac ttc ttc tgc acg gta cct gag atc ctg gtg cac aac ata gtg	737
Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val	
200 205 210 215	
atc ttc atg cga act tca gtg aag att tca tac att ggc ctc atg acc	785
Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr	
220 225 230	
cag agc tcc ttg gag aca cat cac tat gtg gat tgt gga gga aat tcc	833
Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser	
235 240 245	
aca gct att taacaactgc tattggttct tccacacagc gcctgtagaa gagagcac	890
Thr Ala Ile	
250	
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aattggttca cttaactccc agcaaacatc ctccctgccac ttaggaggaa acacctccct	1010
atggtaccat ttatgtttct cagaaccagc agaatcagtg cctagcctgt gccagcaaa	1070
tagttggcac tcaataaaga tttgcagaat ttaatacaga tcttttcagc tgttcttagg	1130
gcattataaa tggaaatcat aacgtgggtc taggttatca aacctggag tgatgtggag	1190
ctaggattgt gagtgacctg caggccatta tcagtgcctc atctgtgcag aagtcgcagc	1250
agagagggac catccaaata cctaagagaa aacagacctc gtcaggatat gaatttgttt	1310
cagctgttcc caaaggcctg ggagcttttt gaaaagaaag aaaaaagtgt gttggctttt	1370
ttttttttta gaaagttaga attgttttta ccaagagtct atgtggggct tgattcacc	1430
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ttc	1493

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Met Gln Ala Pro Ala Phe Arg Asp Lys	
1 5	
aaa cag ggg gtc tca gcc aag aat caa ggt gcc cat gac cca gac tat	100
Lys Gln Gly Val Ser Ala Lys Asn Gln Gly Ala His Asp Pro Asp Tyr	
10 15 20 25	
gag aat atc acc ttg gcc ttc aaa aat cag gac cat gca aag ggt ggt	148
Glu Asn Ile Thr Leu Ala Phe Lys Asn Gln Asp His Ala Lys Gly Gly	
30 35 40	
cat tca cga ccc acg agc caa gtc cca gcc cag tgc agg ccg ccc tca	196
His Ser Arg Pro Thr Ser Gln Val Pro Ala Gln Cys Arg Pro Pro Ser	
45 50 55	
gac tcc acc cag gtc ccc tgc tgg ttg tac aga gcc atc ctg agc ctg	244
Asp Ser Thr Gln Val Pro Cys Trp Leu Tyr Arg Ala Ile Leu Ser Leu	
60 65 70	
tac atc ctc ctg gcc ctg gcc ttt gtc ctc tgc atc atc ctg tca gcc	292
Tyr Ile Leu Leu Ala Leu Ala Phe Val Leu Cys Ile Ile Leu Ser Ala	
75 80 85	
ttc atc atg gtg aag aat gct gag atg tcc aag gag ctg ctg ggc ttt	340
Phe Ile Met Val Lys Asn Ala Glu Met Ser Lys Glu Leu Leu Gly Phe	
90 95 100 105	
aaa agg gag ctt tgg aat gtc tca aac tcc gta caa gca tgc gaa gag	388
Lys Arg Glu Leu Trp Asn Val Ser Asn Ser Val Gln Ala Cys Glu Glu	
110 115 120	
aga cag aag aga ggc tgg gat tcc gtt cag cag agc atc acc atg gtc	436
Arg Gln Lys Arg Gly Trp Asp Ser Val Gln Gln Ser Ile Thr Met Val	

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125	130	135	
agg agc aag att gat aga tta gag acg aca tta gca ggc ata aaa aac			484
Arg Ser Lys Ile Asp Arg Leu Glu Thr Thr Leu Ala Gly Ile Lys Asn			
140	145	150	
att gac aca aag gta cag aaa atc ttg gag gtg ctg cag aaa atg cca			532
Ile Asp Thr Lys Val Gln Lys Ile Leu Glu Val Leu Gln Lys Met Pro			
155	160	165	
cag tcc tca cct caa taaatgagag gacattgtgg cagccaaagc cac			580
Gln Ser Ser Pro Gln			
170			
aacttggaag atggggctgc acctgccaac gaagacggga aatgaccccc cccccagcc			640
tagtgtgaac ctgcccctcg tcccacgtat agaaaaacct cgagtcattgg tgaatgagtg			700
tctcggagtt gctcgtgtgt gtgtacacct gcgtgcgtgt gtgtgcgtgt gtgcgcgtgt			760
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cagtgtatct ccagaaaagg tgatgaatga ataggactga gagtcacagt gaatgtggca			880
tgcattgctg tgtcatgtga catatgtgag tctcggcatg tcacgggtggg tggctgtgtc			940
tgagcacctc cagcagatgt cactctgagt gtgggtgttg gtgacatgca ttgcacgggc			1000
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tgtcatggtg ggggagattt atctccgtac atgtgggtgt cgccatgtgt gccctgtcac			1120
tatctgtggc tgggtgaacg gctgtgtcat tatgagtgtg ccgagttatg ccaccctgtg			1180
tgctcagggc acatgcacac agacatttat ctctgcactc acattttgtg acttatgaag			1240
ataaataaag tcaagggaaa acag			1264